



# WEST

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## Search Results -

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Database: US Patents Full-Text Database	V	•

	14	and	ligating	_	
Refine Search:		***************		T	

## Search History

DB Name	<u>Query</u>	Hit Count	Set Name
USPT	14 and ligating	1	<u>L5</u>
USPT	13 and flanking	34	<u>L4</u>
USPT	12 and ((variable adj number adj tandem adj repeat) or VNTR)	37	<u>L3</u>
USPT	11 and polymorphism	1014	<u>L2</u>
USPT	genomic and tag and fragment and oligonucleotide	3386	<u>L1</u>

1014

3386

<u>L2</u>

<u>L1</u>

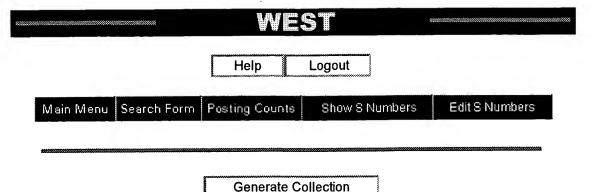
USPT

**USPT** 

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	Help Logout	
	Main Menu   Search Form   Posting Counts   Show S Numbers	Edit 8 Numbers
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	Terms	Documents
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	Search History	
DB Name	<u>Query</u>	Hit Count Set Name
	12 and ((variable adj number adj tandem adj repeat) or VNTR)	37 <u>L3</u>

11 and polymorphism

genomic and tag and fragment and oligonucleotide



### **Search Results -** Record(s) 1 through 37 of 37 returned.

1. Document ID: US 6043031 A

Entry 1 of 37

File: USPT

Mar 28, 2000

US-PAT-NO: 6043031

DOCUMENT-IDENTIFIER: US 6043031 A

TITLE: DNA diagnostics based on mass spectrometry

Full Title Citation Front Review Classification Date Reference Claims KMC Image

2. Document ID: US 6027896 A

Entry 2 of 37

File: USPT

Feb 22, 2000

US-PAT-NO: 6027896

DOCUMENT-IDENTIFIER: US 6027896 A

TITLE: Methods of detecting Alzheimer's disease

Full Title Citation Front Review Classification Date Reference Claims

3 Document ID: US 6027890 A

Entry 3 of 37

File: USPT

Feb 22, 2000

US-PAT-NO: 6027890

DOCUMENT-IDENTIFIER: US 6027890 A

TITLE: Methods and compositions for enhancing sensitivity in the analysis of

biological-based assays

Full Title Citation Front Review Classification Date Reference Claims KMC Image

4. Document ID: US 6013444 A

Entry 4 of 37

File: USPT

Jan 11, 2000

US-PAT-NO: 6013444

DOCUMENT-IDENTIFIER: US 6013444 A

TITLE: DNA bracketing locus compatible standards for electrophoresis

Title Citation Front Review Classification Date Reference Claims KMC Image

5. Document ID: US 5981185 A

Entry 5 of 37

File: USPT

Nov 9, 1999

Record List Display

ı.

US-PAT-NO: 5981185

DOCUMENT-IDENTIFIER: US 5981185 A TITLE: Oligonucleotide repeat arrays

Full Title Citation Front Review Classification Date Reference Claims KMC Image

6. Document ID: US 5952190 A

Entry 6 of 37

File: USPT

Sep 14, 1999

US-PAT-NO: 5952190

DOCUMENT-IDENTIFIER: US 5952190 A

TITLE: cDNA for fanconi anemia complementation group A

Full Title Citation Front Review Classification Date Reference Claims KMC Image

7. Document ID: US 5935787 A

Entry 7 of 37

File: USPT

Aug 10, 1999

US-PAT-NO: 5935787

DOCUMENT-IDENTIFIER: US 5935787 A

TITLE: Detection of hypermutable nucleic acid sequence in tissue

Full Title Citation Front Review Classification Date Reference Claims KMC Image

8. Document ID: US 5919626 A

Entry 8 of 37

File: USPT

Jul 6, 1999

US-PAT-NO: 5919626

DOCUMENT-IDENTIFIER: US 5919626 A

TITLE: Attachment of unmodified nucleic acids to silanized solid phase surfaces

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

9. Document ID: US 5879884 A

Entry 9 of 37

File: USPT

Mar 9, 1999

US-PAT-NO: 5879884

DOCUMENT-IDENTIFIER: US 5879884 A

TITLE: Diagnosis of depression by linkage of a polymorphic marker to a segment of

chromosome 19P13 bordered by D19S247 and D19S394

Full Title Citation Front Review Classification Date Reference Claims KWC Image

10. Document ID: US 5861283 A

Entry 10 of 37

File: USPT

Jan 19, 1999

US-PAT-NO: 5861283

DOCUMENT-IDENTIFIER: US 5861283 A

TITLE: DNA encoding a limbic system-associated membrane protein

Full Title Citation Front Review Classification Date Reference Claims KMC Image

11. Document ID: US 5853988 A

Entry 11 of 37

File: USPT

Dec 29, 1998

US-PAT-NO: 5853988

DOCUMENT-IDENTIFIER: US 5853988 A TITLE: Diagnosis of retinoblastoma

Full Title Citation Front Review Classification Date Reference Claims KMC Image

12. Document ID: US 5853989 A

Entry 12 of 37

File: USPT

Dec 29, 1998

US-PAT-NO: 5853989

DOCUMENT-IDENTIFIER: US 5853989 A

TITLE: Method of characterisation of genomic DNA

Full Title Citation Front Review Classification Date Reference Claims KMC Image

13. Document ID: US 5851769 A

Entry 13 of 37

File: USPT

Dec 22, 1998

US-PAT-NO: 5851769

DOCUMENT-IDENTIFIER: US 5851769 A TITLE: Quantitative DNA fiber mapping

Full Title Citation Front Review Classification Date Reference Claims KWC Image

14. Document ID: US 5849544 A

Entry 14 of 37

File: USPT

Dec 15, 1998

US-PAT-NO: 5849544

DOCUMENT-IDENTIFIER: US 5849544 A

TITLE: Amplification and detection process

Full Title Citation Front Review Classification Date Reference Claims KWC Image

15. Document ID: US 5843660 A

Entry 15 of 37

File: USPT

Dec 1, 1998

US-PAT-NO: 5843660

DOCUMENT-IDENTIFIER: US 5843660 A

TITLE: Multiplex amplification of short tandem repeat loci

Full Title Citation Front Review Classification Date Reference Claims KMC Image

16. Document ID: US 5843669 A

Entry 16 of 37

File: USPT

Dec 1, 1998

US-PAT-NO: 5843669

DOCUMENT-IDENTIFIER: US 5843669 A

TITLE: Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii

FEN-1 endonucleases

Full Title Citation Front Review Classification Date Reference Claims KMC Image

17. Document ID: US 5834183 A

Entry 17 of 37

File: USPT

Nov 10, 1998

US-PAT-NO: 5834183

DOCUMENT-IDENTIFIER: US 5834183 A

TITLE: Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis

Full Title Citation Front Review Classification Date Reference Claims KMC Image

18. Document ID: US 5811233 A

Entry 18 of 37

File: USPT

Sep 22, 1998

US-PAT-NO: 5811233

DOCUMENT-IDENTIFIER: US 5811233 A

TITLE: Compositions and uses thereof in the diagnosis of psoriasis

f psoriasis

many

Full: Title Citation Front Review Classification Date Reference Claims KWC Image

19. Document ID: US 5811235 A

Entry 19 of 37

File: USPT

Sep 22, 1998

US-PAT-NO: 5811235

DOCUMENT-IDENTIFIER: US 5811235 A TITLE: Method of characterisation

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

20. Document ID: US 5795976 A

Entry 20 of 37

File: USPT

Aug 18, 1998

US-PAT-NO: 5795976

DOCUMENT-IDENTIFIER: US 5795976 A

TITLE: Detection of nucleic acid heteroduplex molecules by denaturing

high-performance liquid chromatography and methods for comparative sequencing

Full Title Citation Front Review Classification Date Reference Claims KWC Image

21. Document ID: US 5783666 A

Entry 21 of 37

File: USPT

Jul 21, 1998

US-PAT-NO: 5783666

DOCUMENT-IDENTIFIER: US 5783666 A

TITLE: APC (adenomatous polyosis coli) protein

Full Title Citation Front Review Classification Date Reference Claims KWC Image

22. Document ID: US 5783406 A

Entry 22 of 37

File: USPT

Jul 21, 1998

US-PAT-NO: 5783406

DOCUMENT-IDENTIFIER: US 5783406 A

TITLE: Allelic ladders for short tandem repeat loci

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

23. Document ID: US 5756696 A

Entry 23 of 37

File: USPT

May 26, 1998

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http://jupiter:88/bin/gate.exe?f=TOC&

US-PAT-NO: 5756696

DOCUMENT-IDENTIFIER: US 5756696 A

TITLE: Compositions for chromosome-specific staining

Full Title Citation Front Review Classification Date Reference Claims KMC Image

24. Document ID: US 5753441 A

Entry 24 of 37

File: USPT

May 19, 1998

US-PAT-NO: 5753441

DOCUMENT-IDENTIFIER: US 5753441 A

TITLE: 170-linked breast and ovarian cancer susceptibility gene

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

25. Document ID: US 5747282 A

Entry 25 of 37

File: USPT

May 5, 1998

US-PAT-NO: 5747282

DOCUMENT-IDENTIFIER: US 5747282 A

TITLE: 17Q-linked breast and ovarian cancer susceptibility gene

Full Title Citation Front Review Classification Date Reference Claims KWC Image

26. Document ID: US 5720928 A

Entry 26 of 37

File: USPT

Feb 24, 1998

US-PAT-NO: 5720928

DOCUMENT-IDENTIFIER: US 5720928 A

TITLE: Image processing and analysis of individual nucleic acid molecules

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

27. Document ID: US 5709999 A

Entry 27 of 37

File: USPT

Jan 20, 1998

US-PAT-NO: 5709999

DOCUMENT-IDENTIFIER: US 5709999 A

TITLE: Linked breast and ovarian cancer susceptibility gene

Full Title Citation Front Review Classification Date Reference Claims KMC Image

28. Document ID: US 5691454 A

Entry 28 of 37

File: USPT

Nov 25, 1997

US-PAT-NO: 5691454

DOCUMENT-IDENTIFIER: US 5691454 A

TITLE: APC antibodies

Full Title Citation Front Review Classification Date Reference Claims KMC Image

29. Document ID: US 5681942 A

Entry 29 of 37

File: USPT

Oct 28, 1997

Record List Display

ί.

US-PAT-NO: 5681942

DOCUMENT-IDENTIFIER: US 5681942 A TITLE: Fanconi Anemia Type C gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KMC | Image |

30. Document ID: US 5674686 A

Entry 30 of 37

File: USPT

Oct 7, 1997

US-PAT-NO: 5674686

DOCUMENT-IDENTIFIER: US 5674686 A

TITLE: Allelic ladders for short tandem repeat loci

Full Title Citation Front Review Classification Date Reference Claims KWC Image

31. Document ID: US 5648212 A

Entry 31 of 37

File: USPT

Jul 15, 1997

US-PAT-NO: 5648212

DOCUMENT-IDENTIFIER: US 5648212 A

TITLE: Detection of inherited and somatic mutations of APC gene in colorectal

cancer of humans

Full Title Citation Front Review Classification Date Reference Claims KWC Image

32. Document ID: US 5599666 A

Entry 32 of 37

File: USPT

Feb 4, 1997

US-PAT-NO: 5599666

DOCUMENT-IDENTIFIER: US 5599666 A

TITLE: Allelic ladders for short tandem repeat loci

Full Title Citation Front Review Classification Date Reference Claims KWC Image

33. Document ID: US 5449604 A

Entry 33 of 37

File: USPT

Sep 12, 1995

US-PAT-NO: 5449604

DOCUMENT-IDENTIFIER: US 5449604 A

TITLE: Chromosome 14 and familial Alzheimers disease genetic markers and assays

Full Title Citation Front Review Classification Date Reference Claims KWC Image

34. Document ID: US 5411859 A

Entry 34 of 37

File: USPT

May 2, 1995

US-PAT-NO: 5411859

DOCUMENT-IDENTIFIER: US 5411859 A

TITLE: Genetic identification employing DNA probes of variable number tandem

<u>repeat</u> loci

Full Title Citation Front Review Classification Date Reference Claims KWC Image

35. Document ID: US 5364759 A

Entry 35 of 37

File: USPT

Nov 15, 1994

US-PAT-NO: 5364759

DOCUMENT-IDENTIFIER: US 5364759 A

TITLE: DNA typing with short tandem repeat polymorphisms and identification of

polymorphic short tandem repeats

Full Title Citation Front Review Classification Date Reference Claims KWIC Image

36. Document ID: US 5352775 A

Entry 36 of 37

File: USPT

Oct 4, 1994

US-PAT-NO: 5352775

DOCUMENT-IDENTIFIER: US 5352775 A

TITLE: APC gene and nucleic acid probes derived therefrom

Full Title Citation Front Review Classification Date Reference Claims KMC Image

37. Document ID: US 4963663 A

Entry 37 of 37

File: USPT

Oct 16, 1990

US-PAT-NO: 4963663

DOCUMENT-IDENTIFIER: US 4963663 A

TITLE: Genetic identification employing DNA probes of variable number tandem

repeat loci

Full Title Citation Front Review Classification Date Reference Claims KMC Image

Generate Collection

TermsDocuments12 and ((variable adj number adj tandem adj repeat) or VNTR)37

Display 40 Documents

including document number

Display Format:

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Logout

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Logging in to Dialog
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  File 5:Biosis Previews(R) 1969-2000/Apr W3
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File 399:CA SEARCH(A
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         (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
  File 357: Derwent Biotechnology Abs 1982-2000/Apr B2
          (c) 2000 Derwent Publ Ltd
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Ref Items Index-term
         1 AU=FIRTH, GARY B.
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? t s1/6/1
           (Item 1 from file: 399)
DIALOG(R) File 399:(c) 2000 American Chemical Society. All rts. reserv.
  Extraction of VNTR alleles and detection of polymorphic markers for
inherited traits at multiple loci
? t s1/7/1
           (Item 1 from file: 399)
 1/7/1
DIALOG(R) File 399:CA SEARCH(R)
(c) 2000 American Chemical Society. All rts. reserv.
              CA: 129(21)271497x
                                       PATENT
  129271497
  Extraction of VNTR alleles and detection of polymorphic markers for
inherited traits at multiple loci
  INVENTOR (AUTHOR): Firth, Greg
  LOCATION: UK,
  PATENT: PCT International; WO 9842867 Al DATE: 19981001
  APPLICATION: WO 98GB840 (19980320)
  PAGES: 101 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
  DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN;
CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; GW; HU; ID; IL; IS; JP; KE; KG;
KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL;
PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS
; MW; SD; SZ; UG; ZW; AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU;
MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG
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SECTION:
CA203001 Biochemical
  IDENTIFIERS: VNTR allele isolation TRAIT, polymorphism marker inherited
trait multiple loci
  DESCRIPTORS:
Oligonucleotides...
    double-stranded, phosphorothioate-linked, 3'-blocked; extn. of VNTR
    alleles and detection of polymorphic markers for inherited traits at
    multiple loci
Alleles... Genetic markers... Nucleic acid hybridization...
Polymorphism(genetic)... Primers(nucleic acid)... VNTR(DNA)...
    extn. of VNTR alleles and detection of polymorphic markers for
    inherited traits at multiple loci
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           (Item 1 from file: 399)
DIALOG(R) File 399: (c) 2000 American Chemical Society. All rts. reserv.
  The analysis of aqueous humor constituents using capillary zone
electrophoresis
           (Item 2 from file: 399)
DIALOG(R) File 399:(c) 2000 American Chemical Society. All rts. reserv.
  Studies on the intracerebral injection of vincristine free and entrapped
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within liposomes in the rat

(Item 3 from file: 399). 2/6/3 DIALOG(R) File 399:(c) 2000 American Chemical Society. All rts. reserv.

Studies on the intracerebral injection of bleomycin free and entrapped within liposomes in the rat

(Item 4 from file: 399) DIALOG(R) File 399:(c) 2000 American Chemical Society. All rts. reserv.

Studies on the use of antimitotic drugs entrapped within liposomes and of their action on a human glioma cell line

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2/6/5 (Item 5 from file: 399)
DIALOG(R)File 399: (c) O American Chemical Society. rts. reserv.

Value of measuring serum angiotensin I converting enzyme and serum lysozyme in the management of sarcoidosis
? s variable(w)number(w)tandem(w)repeat
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395106 VARIABLE 1716121 NUMBER 54940 TANDEM 135318 REPEAT 461 VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT ? s variable(w) number(w) tandem(w) repeat(w) allele 395106 VARIABLE 1716121 NUMBER 54940 TANDEM 135318 REPEAT 78041 ALLELE 2 VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT (W) ALLELE ? rd >>>Duplicate detection is not supported for File 654. >>>Records from unsupported files will be retained in the RD set. ...completed examining records S5 2 RD (unique items) ? t s5/6/1-2 (Item 1 from file: 5) 5/6/1 BIOSIS NO.: 199900135530 11889421 Association of ulcerative colitis with rare VNTR alleles of the human intestinal mucin gene, MUC3. 5/6/2 (Item 1 from file: 357) 0230736 DBA Accession No.: 99-00837 Use of variable number tandem repeat allele and their flanking region - for genetic fingerprinting or other method of genotyping individual 1998 ? t s5/7/1-2(Item 1 from file: 5) 5/7/1 DIALOG(R) File 5: Biosis Previews(R) (c) 2000 BIOSIS. All rts. reserv. BIOSIS NO.: 199900135530 Association of ulcerative colitis with rare VNTR alleles of the human intestinal mucin gene, MUC3. AUTHOR: Kyo Kennoki; Parkes Miles; Takei Yoshiki; Nishimori Hiroyuki; Vyas Paulomi; Satsangi Jack; Simmons Jon; Nagawa Hirokazu; Baba Shozo; Jewell

Intestinal much gene, Mucs.

AUTHOR: Kyo Kennoki; Parkes Miles; Takei Yoshiki; Nishimori Hiroyuki; Vyas Paulomi; Satsangi Jack; Simmons Jon; Nagawa Hirokazu; Baba Shozo; Jewell Derek; Muto Tetsuichiro; Lathrop G Mark; Nakamura Yusuke(a)

AUTHOR ADDRESS: (a) Lab. Molecular Med., Human Genome Center, Inst. Medical Science, Univ. Tokyo, 4-6-1, Shirokaneda\*\*Japan

JOURNAL: Human Molecular Genetics 8 (2):p307-311 Feb., 1999

ISSN: 0964-6906

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Ulcerative colitis (UC), a common form of inflammatory bowel disease, is a multifactorial disorder with significant genetic influence.

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Recently, evidence of linkage on chromosome 7q near to intestinal mucin gene MUC3 was report by an affected sib-pair analy. Previous reports indicate a possible mucin abnormality in UC patients, but whether genetic differences in a specific mucin gene are associated with UC is unknown. Here we analysed polymorphisms of variable number of tandem repeats (VNTRs) within this gene using DNAs obtained from 243 Japanese (75 patients with UC and 168 controls), and to confirm the result we undertook a two-stage examination using 328 Caucasian samples (72 and 85 with UC in the first and second stages, respectively, and 171 controls). When the frequency of patients carrying one or two rare VNTR alleles was compared with that of controls, a significant increase was found first in Japanese patients (odds ratio 2.72, 95% CI 1.17-6.32, P = 0.0308). In Caucasians, the odds ratio was 2.80 (95% CI 1.36-5.75, P= 0.0079) in the first stage, 2.43 (95% CI 1.20-4.92, P = 0.0196) in the second stage and 2.60 (95% CI 1.41-4.80, P= 0.0024) in total. The overall odds ratio was 2.64 (95% CI 1.60-4-33, P = 0.0001). This result suggests that rare alleles of the MUC3 gene may confer genetic predisposition to UC.

5/7/2 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0230736 DBA Accession No.: 99-00837 PATENT Use of variable number tandem repeat allele

and their flanking region - for genetic fingerprinting or other method of genotyping individual

AUTHOR: Firth G

CORPORATE SOURCE: Hitchin, UK. PATENT ASSIGNEE: Firth G 1998

PATENT NUMBER: WO 9842867 PATENT DATE: 981001 WPI ACCESSION NO.:

98-609895 (9851)

PRIORITY APPLIC. NO.: EP 97301917 APPLIC. DATE: 970321 NATIONAL APPLIC. NO.: WO 98GB840 APPLIC. DATE: 980320

LANGUAGE: English

ABSTRACT: A method for the extraction of variable number tandem repeat polymorphism (VNTR) alleles is claimed and comprises making a mixture of VNTR alleles and their flanking regions from genomic DNA by: ligating an adaptor to genomic DNA fragments so that the 3' end of the adaptor-terminated fragment is blocked to prevent chain extension, and using these with adaptor-DNA primers and VNTR sense and antisense DNA to generate 3'- and 5'-flanking VNTR amplimers; and using the amplimers as DNA primers to extend on genomic DNA as the template and create the desired mixture of VNTR alleles and their flanking regions. Also claimed are: a method for treating a mixture of polymorphic alleles representative of a desired trait, by separating and re-annealing the DNA strands and discarding mismatches; and a method for identifying an allele-linked to a trait by hybridizing a polymorphic allele representative of the trait with a mixture of non-trait alleles and selecting matches or mismatches to isolate the polymorphic trait-linked allele. The alleles generated can be used for genetic fingerprinting or obtaining selectable markers which segregate with specific traits. (101pp)

? s s1 and polymorphism

1 S1

160329 POLYMORPHISM

S6 1 S1 AND POLYMORPHISM

? t s6/6

6/6/1 (Item 1 from file: 399)

DIALOG(R) File 399:(c) 2000 American Chemical Society. All rts. reserv.

Extraction of VNTR alleles and detection of polymorphic markers for

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(Item 1 from file: 399)
 6/7/1
DIALOG(R) File 399:CA SEARCH(R)
(c) 2000 American Chemical Society. All rts. reserv.
               CA: 129(21)271497x
                                     PATENT
  Extraction of VNTR alleles and detection of polymorphic markers for
inherited traits at multiple loci
  INVENTOR (AUTHOR): Firth, Greg
  LOCATION: UK,
  PATENT: PCT International; WO 9842867 Al DATE: 19981001
  APPLICATION: WO 98GB840 (19980320)
  PAGES: 101 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
  DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN;
CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; HU; ID; IL; IS; JP; KE; KG;
KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL;
PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU;
ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS
; MW; SD; SZ; UG; ZW; AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU;
MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG
  SECTION:
CA203001 Biochemical Genetics
  IDENTIFIERS: VNTR allele isolation TRAIT, polymorphism marker inherited
trait multiple loci
  DESCRIPTORS:
Oligonucleotides...
    double-stranded, phosphorothioate-linked, 3'-blocked; extn. of VNTR
    alleles and detection of polymorphic markers for inherited traits at
   multiple loci
Alleles... Genetic markers... Nucleic acid hybridization...
Polymorphism(genetic)... Primers(nucleic acid)... VNTR(DNA)...
    extn. of VNTR alleles and detection of polymorphic markers for
    inherited traits at multiple loci
? DS
Set
        Items
                Description
                AU="FIRTH, GREG"
S1
            1
S2
            5
                AU="FIRTH, G."
                VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT
S3
          461
S4
                VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT (W) ALLELE
            2
            2
                RD (unique items)
S5
                S1 AND POLYMORPHISM
            1
S6
? s s3 and polymorphism
             461 S3
          160329 POLYMORPHISM
             252 S3 AND POLYMORPHISM
     s7
? s s7 and flanking
             252 S7
           50563 FLANKING
              34 S7 AND FLANKING
      S8
? rd
>>>Duplicate detection is not supported for File 654.
>>>Records from unsupported files will be retained in the RD set.
...completed examining records
              31 RD (unique items)
      S9
? t s9/6/1-31
```

9/6/1 (Item 1 frd lile: 155)

10019865 99303259

Characterization of a **variable number tandem**repeat region in the thiopurine S-methyltransferase gene promoter.
Apr 1999

9/6/2 (Item 2 from file: 155)

09296867 97449816

Products of partial digestion with Hae III. Part 1. Characterization, casework experience and confirmation of the theory of three-, four- and five-banded RFLP pattern origins using partial digestion.

Sep 1997

9/6/3 (Item 3 from file: 155)

06500589 91033793

Rapid diagnosis of Miller-Dieker syndrome and isolated lissencephaly sequence by the polymerase chain reaction.
Oct 1990

9/6/4 (Item 1 from file: 5) 12198641 BIOSIS NO.: 199900493490

Characterization of a variable number tandem repeat

region in the thiopurine S-methyltransferase gene promoter.

9/6/5 (Item 2 from file: 5) 08726704 BIOSIS NO.: 199395016055

Characterization of a porcine variable number tandem

repeat sequence specific for the glucosephosphate isomerase locus.

9/6/6 (Item 3 from file: 5) 07331090 BIOSIS NO.: 000090110992

RAPID DETECTION OF HYPERVARIABLE REGIONS BY THE POLYMERASE CHAIN REACTION TECHNIQUE

1990

9/6/7 (Item 1 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

DNA sequences from specific human genomic loci useful for identification of individuals

9/6/8 (Item 1 from file: 357) 0230736 DBA Accession No.: 99-00837

Use of variable number tandem repeat allele and

their **flanking** region - for genetic fingerprinting or other method of genotyping individual 1998

9/6/9 (Item 1 from file: 654)

03067992

DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR ELECTROPHORESIS

FULL TEXT: 1867 lines

9/6/10 (Item 2 from file: 654)

COMPARATIVE GENOMIC HY DIZATION (CGH)

FULL TEXT: 3594 lines

9/6/11 (Item 3 from file: 654)

03016138

COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

3528 lines FULL TEXT:

9/6/12 (Item 4 from file: 654)

02990978

METHOD OF DIAGNOSING PREDISPOSITION FOR ULCERATIVE COLITIS IN JEWISH POPULATION BY DETECTION OF INTERLEUKIN-1 RECEPTOR ANTAGONIST

POLYMORPHISM

612 lines FULL TEXT:

9/6/13 (Item 5 from file: 654)

02983945

DETECTION OF HYPERMUTABLE NUCLEIC ACID SEQUENCE IN TISSUE

1815 lines FULL TEXT:

9/6/14 (Item 6 from file: 654)

02934815

POLYMORPHIC LOCUS

874 lines FULL TEXT:

9/6/15 (Item 7 from file: 654)

02922010

DIAGNOSIS OF DEPRESSION BY LINKAGE OF A POLYMORPHIC MARKER TO A SEGMENT OF

CHROMOSOME 19P13 BORDERED BY D19S247 AND D19S394

1466 lines FULL TEXT:

9/6/16 (Item 8 from file: 654)

02901617

TRABECULAR MESHWORK INDUCED GLUCOCORTICOID RESPONSE (TIGR) NUCLEIC ACID

MOLECULES

[Accurate glaucoma diagnosis]

1373 lines FULL TEXT:

(Item 9 from file: 654) 9/6/17

02895578

POLYMORPHISMS IN THE GLUCOSE-6 PHOSPHATE DEHYDROGENASE LOCUS

FULL TEXT:

1360 lines

(Item 10 from file: 654) 9/6/18

02895571

COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

[Detection of amplification, reproduction, and, or deletion of genones]

3541 lines FULL TEXT:

(Item 11 from file: 654) 9/6/19

02893542

METHODS FOR THE DIAGNOSIS OF GLAUCOMA

1532 lines FULL TEXT:

9/6/20 (Item 12 from file: 654)

02893131

METHOD OF CHARACTERISATION OF GENOMIC DNA

FULL TEXT: 4623 lines

9/6/21 (Item 13 from file: 654)

02888348

METHODS FOR THE DIAGNOSIS OF GLAUCOMA

FULL TEXT: 1514 lines

9/6/22 (Item 14 from file: 654)

02846423

METHOD OF CHARACTERISATION

[ Amplification of tandemly repeated region of genomic DNA, separation of

set of amplification products to provide sample code]

FULL TEXT: 3543 lines

9/6/23 (Item 15 from file: 654)

02822670

METHODS FOR THE DIAGNOSIS OF GLAUCOMA [Using a glucocorticoid induced protein]

FULL TEXT: 1949 lines

9/6/24 (Item 16 from file: 654)

02750443

COMPARATIVE GENOMIC HYBRIDIZATION

[Detecting abnormal nucleic acid sequence copy numbers in cell population]

FULL TEXT: 2854 lines

9/6/25 (Item 17 from file: 654)

02740190

METHOD OF SELECTING GENETICALLY SUPERIOR SHRIMP

[Screening shrimp and genetic marking, hybridization and isolation of DNA]

FULL TEXT: 791 lines

9/6/26 (Item 18 from file: 654)

02687789

COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

[Labelling DNA sequences, hybridization; diagnosing genetic disorders]

FULL TEXT: 2975 lines

9/6/27 (Item 19 from file: 654)

02623272

METHODS FOR THE DIAGNOSIS OF GLAUCOMA

[ Specific nucleic acid encoded human trabecular meshwork induced

glucocorticoid response protein]

FULL TEXT: 1303 lines

9/6/28 (Item 20 from file: 654)

02409494

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER

TANDEM REPEAT LOCI

FULL TEXT: 2125 lines

9/6/29 (Item 21 from file: 654)

02404991

GENETIC DIAGNOSIS OF TOPSION DYSTONIA FULL TEXT: 2379 nes

9/6/30 (Item 22 from file: 654)

02357021

DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF

POLYMORPHIC SHORT TANDEM REPEATS FULL TEXT: 1738 lines

9/6/31 (Item 23 from file: 654)

01913496

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER

TANDEM REPEAT LOCI

[IDENTIFICATION OF CLONED DNA SEQUENCES]

FULL TEXT: 2145 lines

? t s9/7/1-7

9/7/1 (Item 1 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

10019865 99303259

Characterization of a variable number tandem

repeat region in the thiopurine S-methyltransferase gene promoter.
Spire-Vayron de la Moureyre C; Debuysere H; Fazio F; Sergent E; Bernard C

; Sabbagh N; Marez D; Lo Guidice JM; D'halluin JC; Broly F

Laboratoire de Biochimie et Biologie Moleculaire, Hopital Calmette, Centre Hospitalier Regional et Universitaire, Lille, France.

Pharmacogenetics (ENGLAND) Apr 1999, 9 (2) p189-98, ISSN 0960-314X Journal Code: BRT

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Characterization of the genetic polymorphism of thiopurine S-methyltransferase enzyme (TPMT; EC 2.1.1.67) is required because of its clinical importance for patients exposed to thiopurine drugs. A number of point mutations have already been characterized in exons and introns of the TPMT gene. Here we report the identification of a polymorphic locus within the promoter region of the gene. This polymorphism was detected by polymerase chain reaction - single strand conformation polymorphism analysis of DNA samples from 54 unrelated European individuals. A total of five alleles with length variations were distinguished through the 5'-flanking region involved in the TPMT gene expression. Sequence analysis revealed that these variations were due to a variable number of tandem repeats (VNTR), ranging from four to eight repeats. Each repeat consists of 17 or 18 bp units and contains putative binding sites for transcription factors. The most frequent alleles harbour four or five tandem repeats, a heterozygosity rate of 0.44 was calculated, and a stable Mendelian inheritance of alleles was demonstrated. Analysis of the effect of each VNTR allele on promoter activity of a reporter gene was further performed in various cell lines by transient transfection assay. A modulatory effect of VNTR alleles was observed in vitro, but the repeat polymorphism did not display a significative role in TPMT gene regulation in vivo. Further studies need to be carried out to support the hypothesis that VNTR may contribute to the large interindividual variations of TPMT activity.

9/7/2 (Item 2 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

09296867 97449816

Products of partial digestion with Hae III. Part Characterization, casework experience confirmation of the theory three-, four- and five-banded RFLP pattern origins using partial digestion.

Benzinger EA; Emerek EA; Grigsby NL; Duewer DL; Lovekamp ML; Deadman H; Thompson JL; Sallee PJ; Riech AK

Illinois State Police, Springfield, USA.

J Forensic Sci (UNITED STATES) Sep 1997, 42 (5) p850-63, ISSN 0022-1198 Journal Code: I5Z

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The sizes of Hae III partial digestion products at D1S7, D2S44, D4S139, D5S110, D10S28, and D17S26 were evaluated in experimentally generated partial digestions of liquid blood DNA. The partial digestion products were highly predictable, suggesting a very high level of sequence conservation in regions flanking variable number tandem repeat (VNTR) blocks. Partial digestion bands associated with

repeat (VNTR) blocks. Partial digestion bands associated with three-or-more-banded patterns were also characterized. Partial digestion of three-banded patterns can be used to determine whether the extra bands arise due to internal Hae III sites in the VNTR block and to identify hidden three-banded patterns. Partial digestion products from forensic casework also conformed to size expectations. Presumed partial digestion bands from 27 forensic samples were compared to the experimentally generated data. The causes of partial digestion are examined and recommendations for interpreting forensic DNA evidence exhibiting partial digestion products are given.

5,7,9,14-20

9/7/3 (Item 3 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

06500589 91033793

Rapid diagnosis of Miller-Dieker syndrome and isolated lissencephaly sequence by the polymerase chain reaction.

Batanian JR; Ledbetter SA; Wolff RK; Nakamura Y; White R; Dobyns WB; Ledbetter DH

Institute for Molecular Genetics, Baylor College of Medicine, Houston, TX 77030.

Hum Genet (GERMANY) Oct 1990, 85 (5) p555-9, ISSN 0340-6717

Journal Code: GED

Contract/Grant No.: HD20619, HD, NICHD

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Probe YNZ22 (D17S5) is a highly polymorphic, variable number tandem repeat (VNTR) marker previously shown to be deleted in all patients with the Miller-Dieker syndrome (MDS) but not in patients with isolated lissencephaly sequence (ILS). Primers were constructed to the unique sequence **flanking** the polymorphic, repetitive region of YNZ22 for amplification by the polymerase chain reaction (PCR). Analysis of 118 normal individuals revealed 12 alleles (differing in copy number of a 70-bp repeat unit) ranging in size from 168 to 938 bp. A retrospective study of eight MDS and six ILS patients was consistent with Southern blot analysis in all cases except one. In the latter, a very large allele (12 copies of the repeat unit) in a patient and her mother failed to amplify on initial attempts, but was successfully amplified by reducing the concentration of genomic DNA used in the reaction. Prospective studies on two MDS and five ILS patients were successfully performed and confirmed in all cases by Southern blot analysis. From the total sample, restriction fragment length polymorphism (RFLP) analysis was fully informative in four of ten MDS patients and showed a deletion in all four cases. Nine of eleven ILS patients were heterozygous and therefore not deleted for YNZ22. Development of primers for additional polymorphic markers in the Miller-Dieker region will lead to a rapid PCR-based diagnostic approach for all MDS and ILS patients. PCR typing of YNZ22 will also facilitate use of this marker in other applications, including genetic linkage, paternity and forensic

9/7/4 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

12198641 BIOSIS NO.: 199900493490

Characterization of a variable number tandem repeat

region in the thiopurine S-methyltransferase gene promoter.

AUTHOR: de la Moureyre Catherine Spire-Vayron; Debuysere Herve; Fazio Fanny; Sergent Elodie; Bernard Claudine; Sabbagh Nada; Marez Delphine; Guidice Jean-Marc Lo; D'halluin Jean-Claude; Broly Franck(a)

AUTHOR ADDRESS: (a) Laboratoire de Biochimie et Biologie Moleculaire Hopital Calmette, CHRU de Lille, Boulevard Leclercq, F-59037, Lille Cedex\*\*France JOURNAL: Pharmacogenetics 9 (2):p189-198 April, 1999

ISSN: 0960-314X

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Characterization of the genetic polymorphism of thiopurine S-methyltransferase enzyme (TPMT; EC 2.1.1.67) is required because of its clinical importance for patients exposed to thiopurine drugs. A number of point mutations have already been characterized in exons and introns of the TMPT gene. Here we report the identification of a polymorphic locus within the promoter region of the gene. This polymorphism was detected by polymerase chain reaction - single strand conformation polymorphism analysis of DNA samples from 54 unrelated European individuals. A total of five alleles with length variations were distinguished through the 5'-flanking region involved in the TPMT gene expression. Sequence analysis revealed that these variations were due to a variable number of tandem repeats (VNTR), ranging from four to eight repeats. Each repeat consists of 17 or 18 bp units and contains putative binding sites for transcription factors. The most frequent alleles harbour four or five tandem repeats, a heter ozygosity rate of 0.44 was calculated, and a stable Mendelian inheritance of alleles was demonstrated. Analysis of the effect of each VNTR allele on promoter activity of a reporter gene was further performed in various cell lines by transient transfection assay. A modulatory effect of VNTR alleles was observed in vitro, but the repeat polymorphism did not display a significative role in TPMT gene regulation in vivo. Further studies need to be carried out to support the hypothesis that VNTR may contribute to the large interindividual variations of TPMT activity.

9/7/5 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

08726704 BIOSIS NO.: 199395016055

Characterization of a porcine variable number tandem

repeat sequence specific for the glucosephosphate isomerase locus.

AUTHOR: Davies W(a); Kran S; Kristensen T; Harbitz I

AUTHOR ADDRESS: (a) Dep. Biochem., Norw. Coll. Vet. Med., P.O. Box 8146 Dep,

0033 Oslo 1\*\*Norway

JOURNAL: Animal Genetics 23 (5):p437-441 1992

ISSN: 0268-9146

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: A variable number of tandem repeat from a porcine glucosephosphate isomerase intron has been isolated and sequenced. The

repeat has a unit size of 39 bp, is highly conserved and is present in at least 14 copies. Flaging sequences show a sequence hodicity of 53-54 bp and some sequence homology to the 39 bp repeat. A considerable part of the genomic DNA has been lost during subcloning and is considered to be deletion prone or refractory to propagation in Escherichia coli. The tandem repeat is locus specific and detects at least six alleles in BamHI digested porcine DNA. No homology to other tandem repeat sequences has been found.

9/7/6 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

07331090 BIOSIS NO.: 000090110992

RAPID DETECTION OF HYPERVARIABLE REGIONS BY THE POLYMERASE CHAIN REACTION TECHNIQUE

AUTHOR: DECORTE R; CUPPENS H; MARYNEN P; CASSIMAN J-J

AUTHOR ADDRESS: CENTER HUMAN GENETICS, UNIV. LEUVEN, CAMPUS GASTHUISBERG O AND N6, HERESTRAAT, B-3000 LEUVEN, BELGIUM.

JOURNAL: DNA CELL BIOL 9 (6). 1990. 461-469.

CODEN: DCEBE

RECORD TYPE: Abstract LANGUAGE: ENGLISH

ABSTRACT: The polymerase chain reaction (PCR) technique has provided a substantial improvement for the detection and analysis of known genetic polymorphisms. Here, we describe the application of this method for the detection of variable number of tandem repeat (VNTR) sequences. With the use of unique oligonucleotide primers, flanking the repeat sequence, and the thermostable Taq DNA polymerase, the hypervariable regions 3' of the Ha-ras gene, 3' of the apolipoprotein B gene, and 5' to the joining segments of the heavy-chain immunoglobulin gene could be amplified. Alleles up to 2,000 bp could be visualized directly on ethidium bromide-stained agarose gels. Larger alleles were seen only after traditional Southern blot analysis with an internal probe. The value of this new approach for the detection of VNTRs is illustrated in a case of paternity dispute.

9/7/7 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2000 American Chemical Society. All rts. reserv.

116035667 CA: 116(5)35667p PATENT

DNA sequences from specific human genomic loci useful for identification of individuals

INVENTOR (AUTHOR): Keith, Tim P.; Mao, Jen I; Rose, Stanley D.

LOCATION: USA

ASSIGNEE: Collaborative Research, Inc.

PATENT: PCT International; WO 9110748 Al DATE: 910725

APPLICATION: WO 91US196 (910109) \*US 464960 (900116)

PAGES: 49 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/70A;

C07H-021/04B; G01N-033/53B DESIGNATED COUNTRIES: AU; CA; JP

DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE SECTION:

CA203005 Biochemical Genetics

IDENTIFIERS: oligonucleotide primer DNA VNTR region, hybridization probe DNA VNTR region, human chromosome VNTR primer probe, variable number tandem repeat chromosome primer

DESCRIPTORS:

Nucleotides, oligo-, polymers...

as primers and probes for human chromosome variable no. of tandem repeat regions in DNA identity detn.

Genetic polymorphism...

at variable no. tardem repeat loci, in detn. of DNA mample identities Gene, animal... D1S47, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Gene, animal... D11S129, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Gene, animal... D18S17, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Gene, animal... D20S112, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Gene, animal... D20S15, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Gene, animal... D6S22, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn. Deoxyribonucleic acid sequences... of human chromosome 11 variable no. of tandem repeat locus D11S129, oligonucleotide primers and probes for DNA identity detn. in relation Deoxyribonucleic acid sequences... of human chromosome 6 variable no. of tandem repeat locus D6S22, oligonucleotide primers and probes for DNA identity detn. in relation Nucleic acid hybridization... oligonucleotide probes for, for human chromosome variable no. of tandem repeat regions in DNA identity detn. Deoxyribonucleic acids... polymerase chain reaction amplification of, oligonucleotide primers for, for human chromosome variable no. of tandem repeat regions in DNA identity detn. Gene, animal... variable no. of tandem repeat (VNTR), of human chromosomes, oligonucleotide primer and probes for, for DNA identity detn.

Chromosome, human 1... Chromosome, human 11... Chromosome, human 18... Chromosome, human 20... Chromosome, human 21... Chromosome, human 6... variable no. of tandem repeat region and flanking sequences of, oligonucleotide primers and probes for, DNA identity detn. in relation

CAS REGISTRY NUMBERS:

138363-06-1 138363-07-2 as oligonucleotide primer for sizing of variable amt. of tandem repeat alleles at human chromosome 20 locus D20S15 138363-08-3 138363-09-4 nucleotide sequence of, oligonucleotide primers and probes for DNA identity detn. in relation to ? t s9/3,ab/22, 28, 30, 31

(Item 14 from file: 654) 9/3, AB/22 DIALOG(R) File 654:US Pat. Full. (c) format only 2000 The Dialog Corp. All rts. reserv.

02846423

Utility

METHOD OF CHARACTERISATION

[ Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235

September 22, 1998 (19980922) ISSUED:

INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom). England ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom) England

[Assignee de (s): 32757]

APPL. NO.: 8-418,859

FILED: April 05, 1995 (19950405)

PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)

9119089, GB (United Kingdom), September 6, 1991 (19910906) 9124636, GB (United Kingdom), November 20, 1991 (19911120) 9207379, GB (United Kingdom), April 3, 1992 (19920403) 9212627, GB (United Kingdom), June 15, 1992 (19920615) 9212881, GB (United Kingdom), June 17, 1992 (19920617)

This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT: 3

3543 lines

#### ABSTRACT

A method of characterizing a test sample of genomic DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.

9/3, AB/28 (Item 20 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02409494

Utility

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER TANDEM REPEAT LOCI

PATENT NO.: 5,411,859

ISSUED: May 02, 1995 (19950502)

INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United

States of America)

Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States

of America)

O'Connell, Peter, Salt Lake City, UT (Utah), US (United States

of America)

Midvale, Salt Lake City, UT (Utah), US (United States of

America)

Leppert, Mark F., Salt Lake City, UT (Utah), US (United States

of America)

ASSIGNEE(s): University of Utah Research Foundation, (A U.S. Company or

Corporation), Salt Lake City, UT (Utah), US (United States of

America)

[Assignee Code(s): 88042]

EXTRA INFO: Assignment transaction [Reassigned], recorded April 29,

1998 (19980429)

Assignment transaction [Reassigned], recorded February 26,

1999 (19990226)

APPL. NO.: 7-728,751

FILED: June 10, 1991 (19910610)

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation of application Ser. No. 07-597,039,

filed Oct. 15, 1990, n abandoned, which is divisional of application Ser. No. 07-307,820, filed 8, 1989, now U.S. Pat. No. 3,663, which is a continuation-in-part of application Ser. No. 07-288,835, filed Dec. 23, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-282,141, filed Dec. 9, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-157,962, filed Feb. 18, 1988, now abandoned.

FULL TEXT:

2125 lines

ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize VNTR loci have been isolated from a cosmid library and characterized.

9/3,AB/30 (Item 22 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.

02357021

Utility

DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS

PATENT NO.: 5,364,759

ISSUED: November 15, 1994 (19941115)

INVENTOR(s): Caskey, Charles T., Houston, TX (Texas), US (United States of

America)

Edwards, Albert O., Houston, TX (Texas), US (United States of

America)

ASSIGNEE(s): Baylor College of Medicine, (A U.S. Company or Corporation),

Houston, TX (Texas), US (United States of America)

[Assignee Code(s): 6345]

EXTRA INFO: Reexamined, certified November 18, 1997 (19971118)

Reexamined, certified July 20, 1999 (19990720)

APPL. NO.: 7-647,655

FILED: January 31, 1991 (19910131)

FULL TEXT: 1738 lines

ABSTRACT

The present invention relates to a DNA profiling assay for detecting polymorphisms in a short tandem repeat. The method includes the steps of extracting DNA from a sample to be tested, amplifying the extracted DNA and identifying the amplified extension products for each different sequence. Each different sequence is differentially labeled. In the method, internal and external standards can also be used. The method is applicable to a wide variety of forensic and medical samples, including blood, semen, vaginal swaps, tissue, hair, saliva, urine and mixtures of body fluids. A short tandem repeat sequence which can be characterized by the formula (A sub w G sub x T sub y C sub z) sub n, wherein A, G, T and C represent the nucleotides, w, x, y and z represent the number of nucleotide and range from 0 to 7 and the sum of w+x+y+z ranges from 3 to 7 and n represents the repeat number and ranges from 5 to 50. The labels can be from a variety of groups, including fluorescers, radioisotopes, chemiluminescers, stains, enzymes and antibodies. Also described is a kit. Further, a method of detecting the polymorphic short tandem repeats comprising the steps of either searching for the repeats in a data base or comparing

(Item 23 from file: 654) 9/3,AB/31

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

01913496

Utility

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER

TANDEM REPEAT LOCI

[IDENTIFICATION OF CLONED DNA SEQUENCES]

PATENT NO.: 4,963,663

ISSUED:

October 16, 1990 (19901016)

INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United

States of America)

Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States

of America)

O'Connell, Peter, Midvale, UT (Utah), US (United States of

America)

Leppert, Mark F., Salt Lake City, UT (Utah), US (United States

of America)

ASSIGNEE(s): University of Utah, (A U.S. Company or Corporation), Salt

Lake City, UT (Utah), US (United States of America)

[Assignee Code(s): 88042]

EXTRA INFO: Assignment transaction [Reassigned], recorded March 3,

1992 (19920303)

Assignment transaction [Reassigned], recorded April 29,

1998 (19980429)

Assignment transaction [Reassigned], recorded February 26,

1999 (19990226)

7-307,820

APPL. NO.:

FILED:

February 08, 1989 (19890208)

#### CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation-in-part of application Ser. No. 288,835, filed Dec. 23, 1988 which is a continuation-in-part of application Ser. No. 282,141, filed Dec. 9, 1988 which is a continuation-in-part of application Ser. No. 157,962 filed Feb. 18, 1988.

FULL TEXT:

2145 lines

### ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize VNTR loci have been isolated from a cosmid library and characterized. ? ds

Set	Items	Description
S1	1	AU="FIRTH, GREG"
S2	5	AU="FIRTH, G."
S3	461	VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT
S4	2	VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT (W) ALLELE
<b>s</b> 5	2	RD (unique items)
S6	1	S1 AND POLYMORPHISM
s7	252	S3 AND POLYMORPHISM
S8	34	S7 AND FLANKING

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31
                        we items)
                RD (un
? s amplimer
            438 AMPLIMER
     S10
? s s10 and s3
             438 S10
             461 S3
               2 S10 AND S3
     S11
? t s11/6/1-2
            (Item 1 from file: 654)
 11/6/1
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
                  4623 lines
FULL TEXT:
 11/6/2
            (Item 2 from file: 654)
02846423
METHOD OF CHARACTERISATION
[ Amplification of tandemly repeated region of genomic DNA, separation of
set of amplification products to provide sample code]
                 3543 lines
FULL TEXT:
? t s11/3, ab/1-2
 11/3,AB/1
               (Item 1 from file: 654)
DIALOG(R) File 654:US Pat. Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.
             02893131
Utility
METHOD OF CHARACTERISATION OF GENOMIC DNA
PATENT NO.: 5,853,989
             December 29, 1998 (19981229)
ISSUED:
INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom). Great
             Britian
             Little, Stephen, Chester, GB (United Kingdom). Great Britian
             Ferrie, Richard Mark, Cheshire, GB (United Kingdom). Great
             Britian
             Brownie, Jannine, Cheshire, GB (United Kingdom). Great Britian
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London,
             GB (United Kingdom)
             [Assignee Code(s): 32757]
             8-643,181
APPL. NO.:
             May 06, 1996 (19960506)
FILED:
             9118371, GB (United Kingdom), August 27, 1991 (19910827)
PRIORITY:
             9119089, GB (United Kingdom), September 6, 1991 (19910906)
             9124636, GB (United Kingdom), November 20, 1991 (19911120)
             9207379, GB (United Kingdom), April 3, 1992 (19920403)
             9212627, GB (United Kingdom), June 15, 1992 (19920615)
             9212881, GB (United Kingdom), June 17, 1992 (19920617)
```

This application is a continuation-in-part of application of Ser. No. 08-418,859 filed Apr. 5, 1995 which is a continuation of 07-935,107, filed Aug. 26, 1992 now abandoned.

FULL TEXT: 4623 lines

ABSTRACT

The present invention relates generally to a method of characterizing a sample of genomic DNA and to nucleotide sequences employed in the method as well as kits comprising these. In particular the invention involves the use of primers which selectively prime specific type(s) of internal repeat unit in a tandemly repeated region. The method of the invention is particularly useful in forensic or paternity studies and provides individual sample codes suitable for computerized storage on, and retrieval from, a database.

11/3,AB/2 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.

02846423

Utility

METHOD OF CHARACTERISATION

[ Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235

ISSUED: September 22, 1998 (19980922)

INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom) England ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London,

GB (United Kingdom) England [Assignee Code(s): 32757]

APPL. NO.: 8-418,859

FILED: April 05, 1995 (19950405)

PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827) 9119089, GB (United Kingdom), September 6, 1991 (19910906) 9124636, GB (United Kingdom), November 20, 1991 (19911120) 9207379, GB (United Kingdom), April 3, 1992 (19920403)

9207379, GB (United Kingdom), April 3, 1992 (19920403) 9212627, GB (United Kingdom), June 15, 1992 (19920615) 9212881, GB (United Kingdom), June 17, 1992 (19920617)

This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT:

3543 lines

#### ABSTRACT

A method of characterizing a test sample of genomic DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.

? ds

Set	Items	Description
S1	1	AU="FIRTH, GREG"
S2	5	AU="FIRTH, G."
S3	461	VARIABLE(W) NUMBER(W) TANDEM(W) REPEAT
S4	2	VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT (W) ALLELE
S5	2	RD (unique items)
S6	1	S1 AND POLYMORPHISM
s7	252	S3 AND POLYMORPHISM

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S7 AND TLANKING
           34
S9
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                RD (ur
                         le items)
'S10
          438
                AMPLIMER
S11
            2
                S10 AND S3
? s s3 and genomic
             461
                 s3
          130463 GENOMIC
     S12
              75 S3 AND GENOMIC
? rd
>>>Duplicate detection is not supported for File 654.
>>>Records from unsupported files will be retained in the RD set.
...examined 50 records (50)
...completed examining records
     S13
              61 RD (unique items)
? s s13 not s8
              61
                  S13
              34
                 S8
     S14
              35
                 S13 NOT S8
? t s11/6/1-35
 11/6/1
            (Item 1 from file: 654)
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
FULL TEXT:
                  4623 lines
            (Item 2 from file: 654)
 11/6/2
02846423
METHOD OF CHARACTERISATION
[ Amplification of tandemly repeated region of genomic DNA, separation of
set of amplification products to provide sample code]
                  3543 lines
FULL TEXT:
? t s14/6/1-35
 14/6/1
            (Item 1 from file: 155)
           20081706
10241122
  Analysis of parent-offspring trios provides evidence for linkage and
association
              between the insulin gene and type 2 diabetes mediated
exclusively
             through
                      paternally transmitted class III variable
number tandem repeat alleles.
Jan 2000
            (Item 2 from file: 155)
 14/6/2
           98424414
   Duplication of a genomic region containing the Cdc2L1-2 and
MMP21-22 genes on human chromosome 1p36.3 and their linkage to D1Z2.
Sep 1998
 14/6/3
           (Item 3 from file: 155)
           97311416
09081095
  Gene organization of human NOTCH4 and (CTG)n polymorphism in this human
counterpart gene of mouse proto-oncogene Int3.
Apr 21 1997
```

14/6/4

08927469

(Item 4 from file: 155)

97147788

14/6/5 (Item 5 from file: 155)

08820287 96432029

Two additional polymorphisms within the hypervariable MUC1 gene: association of alleles either side of the VNTR region.

Jan 1996

14/6/6 (Item 6 from file: 155)

08788942 96296999

Thyroid peroxidase: evidence for disease gene exclusion in Pendred's syndrome.

Apr 1996

14/6/7 (Item 7 from file: 155)

08195213 95078843

Early embryonic failure associated with uniparental disomy for human chromosome 21.

Aug 1994

14/6/8 (Item 8 from file: 155)

08090783 95113701

DNA fingerprinting used to test for family effects on precocious sexual maturation in two populations of Oncorhynchus tshawytscha (Chinook salmon). Dec 1994

14/6/9 (Item 9 from file: 155)

08051141 95057304

No evidence for microsatellite instability or consistent loss of heterozygosity at selected loci in chronic myeloid leukaemia blast crisis. Nov 1994

14/6/10 (Item 10 from file: 155)

07445472 93036587

Characterization of a porcine variable number tandem repeat sequence specific for the glucosephosphate isomerase locus. 1992

14/6/11 (Item 11 from file: 155)

07354599 91332029

Molecular cloning and analysis of the mouse homologue of the tumor-associated mucin, MUC1, reveals conservation of potential O-glycosylation sites, transmembrane, and cytoplasmic domains and a loss of minisatellite-like polymorphism.

Aug 15 1991

14/6/12 (Item 12 from file: 155)

07344347 90368715

Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.

Sep 5 1990

14/6/13 (Item 13 from file: 155) 07245699 93145050

Hypervariable single and multi-locus DNA polymorphisms for genetic typing

Parentage determination on placental tissues through deoxyribonucleic acid

BIOSIS NO.: 199497045074

(Item 6 from file: 5)

08947711 BIOSIS NO.: 199396099212

09036704

14/6/22

fingerprints.

1993

of non-human primates.

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14/6/23
            (Item 7 from file: 5)
07498879
         BIOSIS NO.: 000091072748
STRUCTURE AND EXPRESSION OF THE HUMAN POLYMORPHIC EPITHELIAL MUCIN GENE AN
  EXPRESSED VNTR UNIT
1990
 14/6/24
             (Item 8 from file: 5)
06605822 BIOSIS NO.: 000087047984
A MAPPED SET OF GENETIC MARKERS FOR HUMAN CHROMOSOME 9
1988
 14/6/25
             (Item 1 from file: 357)
0201896 DBA Accession No.: 96-12667
Genetic typing by capillary electrophoresis with the allelic ladder as an
    absolute standard - variable number tandem
    repeat polymorphism detection 1996
 14/6/26
             (Item 2 from file: 357)
0148651 DBA Accession No.: 93-06703
A low profile - examination of the use of molecular biology in DNA
    fingerprinting forensics 1993
             (Item 3 from file: 357)
 14/6/27
0102806 DBA Accession No.: 90-05497
Alkaline transfer of small restriction fragments from polyacrylamide gels
- Southern blot hybridization of DNA after polyacrylamide gel
    electrophoresis; application in variable number
    tandem repeat detection 1990
 14/6/28
             (Item 1 from file: 654)
02987652
METHOD FOR CAPTURING A NUCLEIC ACID
                 826 lines
FULL TEXT:
 14/6/29
            (Item 2 from file: 654)
02788987
COMPOSITIONS FOR CHROMOSOME-SPECIFIC STAINING
[Nucleic acid probes for in situ hybridization with labels]
                 3373 lines
FULL TEXT:
            (Item 3 from file: 654)
 14/6/30
02788602
SEQUENCE OF HUMAN DOPAMINE TRANSPORTER CDNA
                 1776 lines
FULL TEXT:
            (Item 4 from file: 654)
 14/6/31
02745507
VNTR PROBES AND METHODS OF USING THEREOF
[Genetic identification]
FULL TEXT:
                 679 lines
 14/6/32
            (Item 5 from file: 654)
02724581
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DETECTING GENETIC PREDISPOSITION FOR OSTEOPOROSIS
[Isolation genomic Dname letermination allelic pattern]
FULL TEXT: 632 lines

14/6/33 (Item 6 from file: 654)

02588755

PROCESS OF SELECTING AND/OR OBTAINING PROBES CAPABLE OF DETECTING NEW VARIABLE NUMBER TANDEM REPEAT REGIONS

FULL TEXT: 727 lines

14/6/34 (Item 7 from file: 654)

02468366

PROCESS FOR TESTING GENE-DISEASE ASSOCIATIONS

FULL TEXT: 1131 lines

14/6/35 (Item 8 from file: 654)

02427349

REPEAT SEQUENCE CHROMOSOME SPECIFIC NUCLEIC ACID PROBES AND METHODS OF PREPARING AND USING

[ Primer directed DNA amplification using degenerate primers to isolate efficiently chromosome-specific repeated DNA]

FULL TEXT: 2094 lines

? t s14/7/1-27

14/7/1 (Item 1 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

10241122 20081706

Analysis of parent-offspring trios provides evidence for linkage and association between the insulin gene and type 2 diabetes mediated exclusively through paternally transmitted class III variable number tandem repeat alleles.

Huxtable SJ; Saker PJ; Haddad L; Walker M; Frayling TM; Levy JC; Hitman GA; O'Rahilly S; Hattersley AT; McCarthy MI

Division of Medicine, Imperial College School of Medicine, St. Mary's Hospital, London, UK.

Diabetes (UNITED STATES) Jan 2000, 49 (1) p126-30, ISSN 0012-1797

Journal Code: E8X
Languages: ENGLISH

Document type: JOURNAL ARTICLE

Variation at the variable number tandem repeat

(VNTR) minisatellite 5' of the insulin gene (INS) is associated with several phenotypes, including type 1 diabetes, polycystic ovary syndrome, and birth weight. Case-control studies have suggested that class III VNTR alleles are also associated with type 2 diabetes, but results have been inconsistent and may reflect population stratification. To explore further the role of the INS-VNTR in type 2 diabetes susceptibility, we used family-based association methods in 155 parent-offspring trios from the British Diabetic Association-Warren Trios repository, each ascertained via a Europid proband with type 2 diabetes. Overall, there was no significant association between diabetes and the INS-VNTR genotype, with 65 of 119 heterozygous parents (55%) transmitting class III and 54 class I (P = 0.16, one-sided). However, whereas maternal transmissions followed Mendelian expectation, there was a marked excess of class III transmission from the 49 heterozygous fathers (34 [69%] vs. 15, P = 0.003 vs. 50% expectation, P= 0.003 vs. maternal transmission). These results confirm that variation within the TH-INS-IGF2 locus, most plausibly at the VNTR itself, influences type 2 diabetes susceptibility. By demonstrating that this effect is mediated exclusively by the paternally derived allele, these findings implicate imprinted genes in the pathogenesis of type 2 diabetes.

14/7/2 (Item 2 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

09709628 98424414

Duplication of a **genomic** region containing the Cdc2L1-2 and MMP21-22 genes on human chromosome 1p36.3 and their linkage to D1Z2.

Gururajan R; Lahti JM; Grenet J; Easton J; Gruber I; Ambros PF; Kidd VJ Department of Tumor Cell Biology, St. Jude Children's Research Hospital, Memphis, Tennessee 38101 USA.

Genome Res (UNITED STATES) Sep 1998, 8 (9) p929-39, ISSN 1088-9051 Journal Code: CES

Contract/Grant No.: GM44088, GM, NIGMS; CA67938, CA, NCI; CA21765, CA, NCI

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Cdc2L1 and Cdc2L2 span approximately 140 kb on human chromosome 1p36.3. The products of the Cdc2L genes encode almost identical protein kinases, the PITSLRE kinases, which have functions that may be relevant to the regulation of transcription/splicing and apoptotic signaling. These genes are deleted/translocated in neuroblastomas with MYCN gene amplification, a subset of malignant melanomas, and in a newly delineated deletion syndrome. Here we report that the p36.3 region of human chromosome 1 consists of two identical genomic regions, each of which contain a Cdc2L gene linked to a metalloprotease (MMP) gene in a tail-to-tail configuration. This duplicated genomic region is also linked tightly to D122, a genetic marker containing a highly polymorphic VNTR (variable number tandem repeat ) consisting of an unusual 40-bp reiterated sequence. Thus, these genes and the polymorphic marker D1Z2 are organized follows: telomere-D1Z2-5'-MMP22-3'-3'-Cdc2L2-5'-5'-Cdc2L1 3'-MMP21-5'-centromere. Remarkably, the introns and exons of Cdc2L1 and Cdc2L2, as well as their flanking regions, are essentially identical. A total of 15 amino acid differences, 12 nonconservative and 3 conservative, can be found in the 773-786 amino acids specified by the various products of the Cdc2L genes. Two separate promoter/5' untranslated (UT) regions, CpG2, are identical to a reported previously methylated and genomic CpG sequence and are used to express >20 different Cdc2L transcripts from the two genes. The expression of CpG2 transcripts from Cdc2L1 and Cdc2L2 is tissue/cell-line specific. CpG1 transcripts are expressed ubiquitously from both genes, with perhaps some bias towards the expression of CpG1 Cdc2L1 mRNAs in certain hematopoietic cells.

14/7/3 (Item 3 from file: 155) DIALOG(R)File 155:MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

09081095 97311416

Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3.

Sugaya K; Sasanuma S; Nohata J; Kimura T; Fukagawa T; Nakamura Y; Ando A; Inoko H; Ikemura T; Mita K

Genome Research Group, National Institute of Radiological Sciences, Anagawa, Chiba-ken, Japan. k sugaya@uexs72.nirs.go.jp

Gene (NETHERLANDS) Apr 21 1997, 189 (2) p235-44, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The cDNA and **genomic** clones for the human counterpart of the mouse mammary tumor gene Int3 were isolated and sequenced. We designated this human major histocompatibility complex (MHC) class III gene as NOTCH4, since very recently, by sequencing cDNA clones, the complete form of the mouse proto-oncogene Int3 has been clarified and named Notch4. The present

human NOTCH4 sequence is the first example of the **ge mic** sequence for the extracellular rition of the mammalian Notch4 and by comparing it with the mouse Notch4 cDNA sequence, the exon/intron organization was clarified. The comparison of the predicted amino acid sequence of human NOTCH4 with those of other Notch homologues of a wide range of species revealed four subfamilies for mammalian Notch. In the protein coding region of human NOTCH4, we found (CTG)n repeats showing a **variable** number tandem repeat (VNTR) polymorphism for different human leukocyte antigen (HLA) haplotypes. Ten genes mapped on 6p21.3, including NOTCH4, were found to have counterparts structurally and functionally similar to those mostly mapped on 9q33-q34, indicating

segmental chromosome duplication during the course of evolution. Similarity

14/7/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

of genes on chromosomes 1, 6, 9 and 19 was also discussed.

08927469 97147788

**Genomic** differentiation among natural populations of orang-utan (Pongo pygmaeus).

Zhi L; Karesh WB; Janczewski DN; Frazier-Taylor H; Sajuthi D; Gombek F; Andau M; Martenson JS; O'Brien SJ

Laboratory of Genomic Diversity, National Cancer Institute, Frederick, Maryland 21702-1201, USA.

Curr Biol (ENGLAND) Oct 1 1996, 6 (10) p1326-36, ISSN 0960-9822

Journal Code: B44
Languages: ENGLISH

Document type: JOURNAL ARTICLE

BACKGROUND: Orang-utans exist today in small isolated populations on the of Borneo (subspecies Pongo pygmaeus pygmaeus) and Sumatra (subspecies P. p. abelii). Although, on the basis of their morphological, behavioral and cytogenetical characteristics, the Bornean and Sumatran orang-utan populations are generally considered as two separate subspecies, there is no universal agreement as to whether their genetic differentiation is sufficient to consider and manage them as species, subspecies or population level taxonomic units. A more precise phylogenetic description would affect many conservation management decisions about captive and free-ranging orang-utans. RESULTS: We analyzed the amount and patterns of molecular genetic variation in orang-utan populations using cellular DNA from locations in Sumatra orang-utans two locations-representing four isolated populations-in Borneo. Genetic and phylogenetic analyses of mitochondrial DNA restriction fragment length polymorphisms, nuclear minisatellite (or variable number tandem repeat ) loci and mitochondrial 16S ribosomal RNA sequences led to three major findings. First, the genetic distance and phylogenetic differentiation between Sumatran and Bornean orang-utans is large, greater than that between the common chimpanzee, Pan troglodytes, and the pygmy chimpanzee or bonobo, Pan paniscus. The genetic distance suggests that the two island subspecies diverged approximately 1.5-1.7 million years ago, well before the two islands separated and long enough for species-level differentiation. Second, there is considerable endemic genetic diversity within the Bornean and Sumatran orang-utan populations, suggesting that they have not experienced recent bottlenecks or founder effects. And third, there is little genetic differentiation among four geographically isolated populations of Bornean orang-utans, consistent with gene flow having occurred between them until recently. CONCLUSIONS: Our results are consistent with the view that the genetic differentiation between Sumatran and Bornean orang-utans has reached the level of distinct species. Furthermore, our findings indicate that there is not a genetic imperative for the separate management of geographically isolated Bornean populations.

14/7/5 (Item 5 free file: 155) DIALOG(R)File 155:MEDIC (R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

08820287 96432029

Two additional polymorphisms within the hypervariable MUC1 gene: association of alleles either side of the VNTR region.

Pratt WS; Islam I; Swallow DM

MRC Human Biochemical Genetics Unit, Galton Laboratory (UCL), London, U.K.

Ann Hum Genet (ENGLAND) Jan 1996, 60 ( Pt 1) p21-28, ISSN 0003-4800 Journal Code: 58C

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The gene MUC1 codes for a mucin-type glycoprotein and like most of the other mucin genes shows variable number tandem repeat (VNTR) polymorphism within the coding region. A polymorphism due to a G/A substitution in exon 2, responsible for a genetically determined variation in splicing of the MUC1 transcript, has also been reported (Ligtenberg et al. 1990, 1991). Here we describe the detection of this nucleotide substitution polymorphism by single stranded conformational analysis of genomic DNA and we also report a CA repeat polymorphism within intron 6 of the gene. Haplotypes were determined in a series of families and the common alleles of these two polymorphisms were found to be associated. These results support the notion that the VNTR polymorphism in the coding sequence of MUC1 is not caused by unequal reciprocal recombination at meiosis.

14/7/6 (Item 6 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

08788942 96296999

Thyroid peroxidase: evidence for disease gene exclusion in Pendred's syndrome.

Gausden E; Armour JA; Coyle B; Coffey R; Hochberg Z; Pembrey M; Britton KE; Grossman A; Reardon W; Trembath R

Department of Genetics, University of Leicester, UK.

Clin Endocrinol (Oxf) (ENGLAND) Apr 1996, 44 (4) p441-6, ISSN 0300-0664 Journal Code: DCI

Languages: ENGLISH

Document type: JOURNAL ARTICLE

OBJECTIVE: Pendred's syndrome is an association between congenital neurosensory deafness and goitre with abnormal discharge of iodide following perchlorate challenge, indicating a defect of iodide organification. Although Pendred's syndrome may cause up to 7.5% of all cases of congenital deafness, the molecular basis of the association between the hearing loss and the thyroid organification defect remains unknown. We chose to investigate the role of the thyroid peroxidase (TPO) gene as the genetic defect in Pendred's syndrome. DESIGN: A highly informative variable number tandem repeat (VNTR),

located 1.5 kb downstream of exon 10 of the TPO gene, was used to search for genetic linkage in multiple sibships affected by Pendred's syndrome. PATIENTS: Seven kindreds were recruited from the UK, each with at least two affected members. We have also examined a large inbred Israeli family with two affected offspring and five unaffected children. MEASUREMENTS: Individuals were assigned affected status based on the characteristic clinical features of Pendred's syndrome, namely the presence of congenital sensorineural hearing loss and the appearance in early life of a goitre. Additionally, at least one affected member from each sibship had a characteristic positive perchlorate discharge test (Morgans & Trotter, 1958). PCR amplification of genomic DNA at the TPO VNTR allowed assignment of genotypes to each individual and the calculation of a two-point LOD score. RESULTS: In six of the nine sibships analysed we found

obligatory recombination between TPO and Fordred's syndrome. Non-complementation of eved in affected parents with affected offspring excluded TPO in an affected sibship with genotype sharing and supports a hypothesis of genetic homogeneity for Pendred's syndrome. In two sibships, mutation of the TPO gene as the cause of Pendred's syndrome could not be excluded. CONCLUSIONS: These data suggest that defects at the thyroid peroxidase locus on chromosome 2 are not the major cause of Pendred's syndrome.

14/7/7 (Item 7 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

08195213 95078843

Early embryonic failure associated with uniparental disomy for human chromosome 21.

Henderson DJ; Sherman LS; Loughna SC; Bennett PR; Moore GE

Action Research Laboratory for the Molecular Biology of Fetal Development, Royal Postgraduate Medical School, Queen Charlotte's and Chelsea Hospital, London, UK.

Hum Mol Genet (ENGLAND) Aug 1994, 3 (8) p1373-6, ISSN 0964-6906

Journal Code: BRC

Languages: ENGLISH

Document type: JOURNAL ARTICLE

As many as 16% of all recognized pregnancies may be anembryonic, with failure of the embryo at a very early stage of development leaving only the extraembryonic components of the conceptus to proliferate. Studies in the mouse have shown that the maternal and paternal contributions to the genome of the zygote are not functionally equivalent, due to parental genomic imprinting. Uniparental disomy can reveal imprinting effects,

as in this phenomenon both members of a chromosome pair are inherited from the same parent. We have carried out a systematic search for uniparental disomy in tissues from 23 cases of early embryonic failure, using variable number tandem repeat (VNTR) analysis and

PCR amplification of polymorphic short sequence repeats. Two cases of maternal uniparental heterodisomy for chromosome 21 were identified. One case occurred in conjunction with trisomy for chromosomes 7 and 9, but in the other case maternal uniparental heterodisomy for chromosome 21 was the only chromosomal abnormality found. We therefore postulate that there may be developmentally important genes on human chromosome 21 which are imprinted such that both parental copies are essential for normal embryogenesis.

14/7/8 (Item 8 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

08090783 95113701

DNA fingerprinting used to test for family effects on precocious sexual maturation in two populations of Oncorhynchus tshawytscha (Chinook salmon). Heath DD; Iwama GK; Devlin RH

Department of Animal Science, University of British Columbia, Vancouver, Canada.

Heredity (ENGLAND) Dec 1994, 73 ( Pt 6) p616-24, ISSN 0018-067X Journal Code: G6N

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Two single locus Variable Number Tandem Repeat

(VNTR) DNA probes were used to test for differences in allele distribution between precociously mature male and immature chinook salmon, Oncorhynchus tshawytscha. Two populations were examined: Robertson Creek (RC) adult salmon, and Nicola River (NR) freshwater juveniles, or parr. Genomic DNA was extracted from 74 RC precociously mature adult males ('jacks') and

94 RC immature adult of the same age and from 45 NP recociously mature parr and 51 NR nonmating parr. The **genomic** DNA was included with a single locus VNTR probe developed for chinook salmon (OtSL1), as well as one developed for Atlantic salmon, Salmo salar (Ssal). The allele frequency distributions at both loci were significantly different for the RC jacks and immature fish, indicating a family effect on the incidence of precocious maturation in that population. No difference was found between the allele frequency distribution of the NR precocious and immature parr. A bin width sensitivity analysis showed that the comparisons of the allele frequency distributions were insensitive to the choice of bin size. No differences in heterozygosity were found between mature and immature fish at either locus for both stocks. Preliminary testing for family effects on phenotypes of interest, such as alternative life history strategies, can be performed using hypervariable VNTR DNA probes, prior to implementing costly and involved breeding programmes.

14/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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08051141 95057304

No evidence for microsatellite instability or consistent loss of heterozygosity at selected loci in chronic myeloid leukaemia blast crisis. Silly H; Chase A; Mills KI; Apfelbeck U; Sormann S; Goldman JM; Cross NC LRF Centre for Adult Leukaemia, Royal Postgraduate Medical School, London, UK.

The aim of the present study was to investigate loss of heterozygosity

Leukemia (ENGLAND) Nov 1994, 8 (11) p1923-8, ISSN 0887-6924

Journal Code: LEU Languages: ENGLISH

Document type: JOURNAL ARTICLE

or microsatellite instability in chronic myeloid leukaemia (CML) blast crisis at genomic locations which are known or postulated to harbour tumour suppressor genes. We studied 48 patients in blast crisis of myeloid (n = 31), lymphoid (n = 15), megakaryocytic (n = 1), or mixed lineage (n = 1) phenotype by comparing constitutional DNA extracted from buccal epithelial cells or chronic phase leucocytes with DNA obtained from blast crisis leucocytes. Twelve variable number tandem loci from six different chromosomes were amplified by polymerase chain reaction using labelled primers, and fractionated on polyacrylamide gels. After autoradiography, length as well as intensity of the amplified products were compared between constitutional and blast crisis samples. LOH was scored as complete, partial or none in informative patients. Complete LOH was found in one patient at 8p22 and another at 13q14; partial LOH was detected in three patients at 11p13 and/or 11p15. No LOH was found at 6q27, 8p21, 18q21, 22q11-12 and 22q13 in any patient. Furthermore, no consistent difference in allelic length was observed in 517 paired amplifications indicating no microsatellite instability. We conclude that the Rb gene at 13q14, the Wilms tumour gene at 11p13, the DCC gene at 18q21, the neurofibromatosis 2 gene at 22q11-13 and uncloned tumour suppressor genes at 6q27, 8p21-22 and 11p15, as well as genes responsible for microsatellite instability, are unlikely to be involved in the progression of CML to blast crisis in the majority of patients.

14/7/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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07445472 93036587

Characterization of a porcine **variable number tandem repeat** sequence specific for the glucosephosphate isomerase locus.

Davies W; Kran S; Kristensen T; Harbitz I

Department of Biochemistry, Norwegian College of Veterinary Medicine,

Journal Code: 4WE

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A variable number of tandem repeat from a porcine glucosephosphate isomerase intron has been isolated and sequenced. The repeat has a unit size of 39 bp, is highly conserved and is present in at least 14 copies. Flanking sequences show a sequence periodicity of 53-54 bp and some sequence homology to the 39 bp repeat. A considerable part of the genomic DNA has been lost during subcloning and is considered to be deletion prone or refractory to propagation in E. coli. The tandem repeat is locus specific and detects at least six alleles in BamHI digested porcine DNA. No homology to other tandem repeat sequences has been found.

(Item 11 from file: 155) 14/7/11 DIALOG(R) File 155: MEDLINE(R)

(c) format only 2000 Dialog Corporation. All rts. reserv.

07354599 91332029

Molecular cloning and analysis of the mouse homologue of the tumor-associated mucin, MUC1, reveals conservation of potential O-glycosylation sites, transmembrane, and cytoplasmic domains and a loss of minisatellite-like polymorphism.

Spicer AP; Parry G; Patton S; Gendler SJ

Molecular Epithelial Cell Biology Laboratory, Imperial Cancer Research Fund, London, United Kingdom.

J Biol Chem (UNITED STATES) Aug 15 1991, 266 (23) p15099-109, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We present here the full-length cDNA sequence and genomic structure of the mouse homologue of the tumor-associated mucin, MUC1. This mucin (previously called polymorphic epithelial mucin) is present at the apical surface of most glandular epithelial cells. The mouse gene, Muc-1, encodes an integral membrane protein with 40% of its coding capacity made up of serine, threonine, and proline, a composition typical of a highly The mucin core protein consists of an O-glycosylated protein. amino-terminal signal sequence, a tandem repeat domain encoding 16 repeats of 20-21 amino acids, and unique sequence containing transmembrane and cytoplasmic domains. Homology with the human protein is only 34% in the tandem repeat domain, mainly showing conservation of serines and threonines, presumed sites of O-linked carbohydrate attachment. Homology rises to 87% in the transmembrane and cytoplasmic domains, suggesting that these regions may be functionally important. The pattern of expression of the mouse mucin is very similar to that of its human counterpart and accordingly the two promoter regions share high homology, 74%, although previously identified potential hormone-responsive elements are not conserved. Interestingly, the mouse homologue, unlike its human counterpart does not exhibit a variable number tandem repeat

polymorphism. We present evidence that suggests that the mouse gene was at one time polymorphic but has mutated away from this state.

14/7/12 (Item 12 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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07344347 90368715

Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.

Gendler SJ; Lancaster CA; Taylor-Papadimitriou J; Duhig T; Peat N; Burchell J; Pemberton L; Lalani EN; Wilson D

Imperial Cancer Research Fund, Lincoln's Inn Fields, London, United

Kingdom.

J Biol Chem (UNITH STATE 021-9258 Journal Code: HIV STATES) Sep 5 1990, 265 p15286-93, ISSN

0021-9258

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Human mammary cells present on the cell surface a polymorphic epithelial mucin (PEM) which is developmentally regulated and aberrantly expressed in tumors. PEM carries tumor-associated epitopes recognized by the monoclonal antibodies HMFG-1, HMFG-2, and SM-3. Previously isolated partial cDNA clones revealed that the core protein contained a large domain consisting variable numbers of 20-amino acid repeat units. We now report the full sequence for PEM, as deduced from cDNA sequences. The encoded protein consists of three distinct regions: the amino terminus consisting of a putative signal peptide and degenerate repeats; the major portion of the protein which is the tandem repeat region; the carboxyl terminus consisting degenerate tandem repeats and a unique sequence containing a transmembrane sequence and a cytoplasmic tail. Potential O-glycosylation sites (serines or threonines) make up more than one-fourth of the amino acids. Length variations in the tandem repeat result in PEM being an expressed variable number tandem repeat locus.

Tandem repeats appear to be a general characteristic of mucin core proteins.

(Item 13 from file: 155) 14/7/13

DIALOG(R) File 155: MEDLINE(R)

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93145050

Automated DNA profiling by fluorescent labeling of PCR products.

Sullivan KM; Pope S; Gill P; Robertson JM

Central Research and Support Establishment, Forensic Science Service, Reading, Berks, UK.

Appl (UNITED STATES) Aug 1992, 2 (1) p34-40, ISSN Methods Journal Code: BNV 1054-9803

Languages: ENGLISH

Document type: JOURNAL ARTICLE

DNA profiling has been automated by the fluorescent tagging of amplified variable number tandem repeat (VNTR) loci. This was

achieved by the use of fluorescently labeled primers in the amplification of 10 ng of genomic DNA, coupled with laser detection of the products during electrophoresis. The PCR products are sized by co-electrophoresing a standard size ladder mixed with every sample, thereby eliminating errors in size estimation caused by lane-to-lane differences in migration rate. This increases the precision of VNTR characterization and enables alleles that differ by a single 15-bp repeat to be resolved. The system is capable of high throughput: Twenty-four samples are electrophoresed and analyzed within 6 hr. Also, because four different dyes are available, three different loci can be simultaneously characterized with the fourth dye used for the internal standard. Approximately 100 unrelated British caucasians were analyzed at the loci D1S80, D17S5, and ApoB. The probabilities of two unrelated individuals matching by chance (pM) at these three loci were determined to be 0.065, 0.040, and 0.069, respectively, with a combined pM of  $1.8 \times 10(-4)$ .

(Item 14 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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06824327 92043591

Analytical DNA fingerprinting in lions: parentage; genetic diversity, and kinship.

Gilbert DA; Packer C; Pusey AE; Stephens JC; O'Brien SJ

Biological Carcinogenesis and Development Program, Program Resources,

Inc./DynCorp, NCI-Francerick Cancer Research and velopment Center, Maryland 21702-1201.

J Hered (UNITED STATES) Sep-Oct 1991, 82 (5) p378-86, ISSN 0022-1503

Journal Code: IC7

Contract/Grant No.: NO1-CO-74102, CO, NCI

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The application of hypervariable minisatellite genomic families to the reconstruction of population genetic structure holds great promise in describing the demographic history and future prospects of free-ranging populations. This potential has not yet been realized due to unforeseen empirical constraints associated with the use of heterologous species probes, to theoretical limitations on the power of the procedure to track genic heterozygosity and kinship, and to the absence of extensive field studies to test genetic predictions. We combine here the technical development of feline-specific VNTR (variable number tandem repeat) families of genetic loci with the long-term demographic and behavioral observations of lion populations of the Serengeti ecosystem in East Africa. Minisatellite variation was used to

demographic and behavioral observations of lion populations of the Serengeti ecosystem in East Africa. Minisatellite variation was used to quantify the extent of genetic variation in several populations that differed in their natural history and levels of inbreeding. Definitive parentage, both maternal and paternal, was assessed for 78 cubs born in 11 lion prides, permitting the assessment of precise genealogical relationships among some 200 lions. The extent of DNA restriction fragment sharing between lions was empirically calibrated with the coefficient of relatedness, r, in two different populations that had distinct demographic histories. The results suggest that reliable estimates of relative genetic diversity, of parentage, and of individual relatedness can be achieved in free-ranging populations, provided the minisatellite family is calibrated in established pedigrees for the species.

14/7/15 (Item 15 from file: 155) DIALOG(R)File 155:MEDLINE(R)

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06374849 90196701

Use of multiallelic human DNA probes to detect polymorphisms in the porcine genome.

Troyer DL; Smith JE; Leipold HW

Department of Anatomy and Physiology, College of Veterinary Medicine, Kansas State University, Manhattan 66506.

Am J Vet Res (UNITED STATES) Mar 1990, 51 (3) p479-81, ISSN 0002-9645 Journal Code: 40C

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Two human variable-number tandem repeat probes,

pYNH24 and pYNA23, were examined for their possible ability to detect polymorphisms in the porcine genome. Useful DNA polymorphisms were detected in the porcine species, using both probes. In addition, results of Southern blot analysis of these markers in family studies indicated that the genome fragments obey mendelian laws of inheritance.

14/7/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

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05811008 89372155

Enzymatic synthesis of DNA probes complementary to a human variable number tandem repeat locus.

Ali S; Wallace RB

Department of Molecular Biochemistry, Beckman Research Institute of the City of Hope, Duarte, California 91010.

Anal Biochem (UNITED STATES) Jun 1989, 179 (2) p280-3, ISSN 0003-2697

Journal Code: 4NK

Contract/Grant No.: 3672, CA, NCI

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Both cloned and synthetic DNA probes complementary to human variable number tandem repeat (VNTR) loci have been used to detect restriction fragment length polymorphism. In this report, we describe an approach for the enzymatic synthesis of a DNA probe complementary to one VNTR locus. The probe is produced by annealing short

complementary to one VNTR locus. The probe is produced by annealing short synthetic oligonucleotides comprising single repeat units and enzymatically ligating them into a polymeric DNA probe. In HinfI digests of human genomic DNA separated by agarose gel electrophoresis, this ligated oligonucleotide probe (LOP) detects multiple polymorphic loci in the range of 3-23 kb producing highly informative DNA fingerprint patterns when different individuals are compared. The hybridization pattern is very stable even under high-stringency wash conditions. The LOP is more easily generated than cloned VNTR probes and is totally synthetic, avoiding problems associated with cloned probes including bacterial growth and maintenance as well as in vitro labeling.

14/7/17 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11666796 BIOSIS NO.: 199800448527

VNTR (variable number of tandem repeat) sequences as transcriptional, translational, or functional regulators.

AUTHOR: Nakamura Yusuke(a); Koyama Kumiko; Matsushima Mieko

AUTHOR ADDRESS: (a) Lab. Mol. Med., Hum. Genome Cent., Inst. Med. Sci.,

Univ. Tokyo, 4-6-1 Shirokanedai, Minato-ku, \*\*Japan JOURNAL: Journal of Human Genetics 43 (3):p149-152 1998

ISSN: 1434-5161

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: VNTR (variable number of tandem repeat) markers, also called single-copy minisatellites, were originally isolated from human DNA as highly informative restriction fragment length polymorphisms for mapping purposes. Evidence has lately emerged that some VNTR 'sequences play significant roles in the regulation of transcription, and that some may also influence the translational efficiency or stability of mRNA, or modify the activity of proteins by altering their structure. Some apparent associations of VNTR sequences with personality traits or with susceptibility to diseases have strengthened the likelihood that these tandemly-repeated genomic elements are of physiological and biological importance. In this review, we summarize recent progress in efforts to clarify mechanisms involving VNTR sequences.

14/7/18 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11521469 BIOSIS NO.: 199800302801

Genetic relationships among Japanese, Northern Han, Hui, Uygur, Kazakh, Greek, Saudi Arabian, and Italian populations based on allelic frequencies at four VNTR (D1S80, D4S43, COL2A1, D17S5) and one STR (ACTBP2) loci.

AUTHOR: Katsuyama Yoshihiko; Inoko Hidetoshi; Imanishi Tadashi; Mizuki Nobuhisa; Gojobori Takashi; Ota Masao(a)

AUTHOR ADDRESS: (a) Dep. Legal Med., Shinshu University Sch. Med., Matsumoto, Nagano\*\*Japan

JOURNAL: Human Heredity 48 (3):p126-137 May-June, 1998

ISSN: 0001-5652
DOCUMENT TYPE: Article
'RECORD TYPE: Abstract

RECORD TYPE: Absti

ABSTRACT: The genetic polymorphism at four variable number of tandem repeats (D1S80, D4S43, COL2A1, D17S5) and one short tandem repeat (ACTBP2) loci was assessed by polymerase chain reaction analysis of genomic DNA obtained from blood samples of eight human populations (Japanese, Northern Han, Hui, Uygur, Kazakh, Saudi Arabian, Greek, Italian). Allele frequencies at all loci were in the Hardy-Weinberg equilibrium for each population. With the exception of ACTBP2, the allelic distribution patterns for these loci revealed a marked genetic divergence among the eight populations. A dendrogram constructed by the neighbor-joining method based on the allele frequencies of the five loci suggested that the five Asian populations (Japanese, Northern Han, Hui, Uygur, and Kazakh) formed one cluster, whereas the two European populations and one West Asian population (Italian, Greek, and Saudi Arabian) formed another. The genetic relationship among these populations may have been greatly influenced by admixture as a result of the migration of individuals along the Silk Road throughout history.

14/7/19 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11006345 BIOSIS NO.: 199799627490

Usefulness of intron 40 variable number tandem repeats (VNTR) in gene tracking 14 families with type 1 and 3 von Willebrand disease.

AUTHOR: Surdhar G K; Enayat M S; Theophilus Db D M; Williams D M; Hill F G

AUTHOR ADDRESS: Haematol. Dep., Children's Hosp. NHS Trust, Birmingham\*\*UK JOURNAL: British Journal of Haematology 97 (SUPPL. 1):p85 1997 CONFERENCE/MEETING: Annual Scientific Meeting of the British Society for Haematology Harrogate, England, UK April 14-17, 1997

ISSN: 0007-1048

RECORD TYPE: Citation LANGUAGE: English

14/7/20 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10753435 BIOSIS NO.: 199799374580

DNA allelic alterations within VNTR loci of scleroderma families.

AUTHOR: Artlett C M(a); Black C M; Briggs D C; Stephens C; Welsh K I

AUTHOR ADDRESS: (a)Dep. Rheumatology, Room 522 BLSB, Thomas Jefferson
Univ., Philadelphia, PA 19107\*\*USA

JOURNAL: British Journal of Rheumatology 35 (12):p1216-1222 1996

ISSN: 0263-7103 RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: We have characterized genetic alterations at the molecular level in 49 scleroderma and 45 control families using variable number tandem repeats (VNTRs). Additionally, paired fibroblast cell lines from the 'affected' and 'unaffected' skin and peripheral blood leucocytes of 30 patients were also examined. All families in this study were typed for Class I Cw alleles and Class 11-DRB, -DQA and -DQB to confirm family membership. There were significant rises in the level of VNTR mutations in scleroderma patients (36.7%, n = 18), their siblings (16.3%, n = 13) and offspring (21.7%, n = 15). The level of VNTR mutations in the control group was 0.6% (n = 5). These mutations did not correlate with the

presence of autoantic dies and no patient was taking known clastogenic drug. The most common NTR site for mutation was pyne (17p13.4). Differences were also seen in the VNTR alleles between fibroblast and lymphocyte DNA from the same patient, as measured by size alteration of one of the alleles. We have found that VNTRs are unstable in scleroderma patients, relatives and offspring. The reason for the **genomic** changes remains unknown, but previous studies have implicated the presence of a clastogen.

14/7/21 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09036704 BIOSIS NO.: 199497045074

Hypervariable single and multi-locus DNA polymorphisms for genetic typing of non-human primates.

AUTHOR: Wickings E Jean

AUTHOR ADDRESS: Primate Cent., CIRMF, BP 769, Franceville, Gabon\*\*USA

JOURNAL: Primates 34 (3):p323-331 1993

ISSN: 0032-8332

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: The series of hypervariable, "minisatellite" loci characterized by JEFFREYS and coworkers in the human myoglobin gene have proved to be DNA sequences highly conserved throughout the eukaryotic genome, and hence the methodology developed for human DNA "fingerprinting" has found immediate application in an ever expanding number of species. Primatologists have not been slow to profit from a method which predicts individual recognition to a very high degree of probability, and initial studies have focused on paternity allocation (rather than paternity exclusion, as designated by the classical biochemical markers), adaptive aspects of socio-sexual behaviour patterns and mating systems. A number of probes with sequences corresponding to the common minisatellite core sequences have been used for probing genomic DNA, and synthetic, G-rich oligonucleotides (15-37 bases), corresponding to the core sequence of the minisatellite repeat unit, or simply di-, tri-, or tetranucleotide repeats, appear to be equally discriminatory. The multiple banding patterns produced on hybridization of these probes to restriction enzyme digests of DNA provide an advantage in that the probability of two unrelated individuals sharing the same banding pattern will be low. However, the uncertainty of linkage of the multiple loci identified precludes genotyping and population genetic analyses based on allele frequencies. In contrast, single locus analysis allows DNA typing using variable number tandem repeat (VNTR) or restriction fragment length (RFLP) DNA polymorphisms, and the merits and drawbacks relative to DNA fingerprinting are discussed. For the behavioural primatologists dealing with defined, accessible troops of primates, the value of multilocus DNA fingerprinting, in terms of established methodology and availability of probes applicable to species as phylogenetically wide-ranging as apes and prosimians, may well outweigh the loss of genotypic and population structure data.

14/7/22 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08947711 BIOSIS NO.: 199396099212

Parentage determination on placental tissues through deoxyribonucleic acid fingerprints.

AUTHOR: Jiang Xian-Hua(a); Wei Y

AUTHOR ADDRESS: (a) No. 2 Qishanzhong Rd., Huanggu District, Shenyang \*\* China

JOURNAL: Annals Academ of Medicine Singapore 22 (1):p 10 1993

ISSN: 0304-4602

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: Investigation of **genomic** polymorphisms detected by a mini-satellite "Myo" probe gives distinct and different Deoxyribonucleic Acid (DNA) fingerprints of chorionic villus and decidual membrane in the same placenta. The chorionic villus, which is regarded as the extraembryonal tissue, represents the essential embryonal DNA fingerprint pattern, while the decidual membrane reveals the maternal pattern. A comparison between the DNA fingerprints from the chorionic villus and from the blood sample of the suspected father provides the possibility of setting a paternity test in the early gestational state. Twenty-eight cases of paternity test on aborted placental tissues by DNA fingerprints were analysed.

14/7/23 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07498879 BIOSIS NO.: 000091072748

STRUCTURE AND EXPRESSION OF THE HUMAN POLYMORPHIC EPITHELIAL MUCIN GENE AN EXPRESSED VNTR UNIT

AUTHOR: LANCASTER C A; PEAT N; DUHIG T; WILSON D; TAYLOR-PAPADIMITRIOU J; GENDLER S J

AUTHOR ADDRESS: IMPERIAL CANCER RES. FUND, P.O. BOX 123, LINCOLN'S INN FIELD, LONDON WC2A3PX, UK.

JOURNAL: BIOCHEM BIOPHYS RES COMMUN 173 (3). 1990. 1019-1029.

FULL JOURNAL NAME: Biochemical and Biophysical Research Communications

CODEN: BBRCA

RECORD TYPE: Abstract LANGUAGE: ENGLISH

ABSTRACT: The human polymorphic epithelial mucin (PEM) is expressed apically by glandular epithelium and by the carcinomas that develop from these tissues. Previously isolated cDNA clones revealed that the core protein contained a large domain consisting of variable numbers of 60 bp tandem repeats (TR), making it an expressed minisatellite. We now report the full **genomic** sequence of the PEM gene, including 803 bp of 5'flanking sequence. The gene is composed of 7 exons and varies in size from .apprxeq.4 to .apprxeq.7 kb, depending on the number of tandem repeats in exon 2. Expression of PEM was obtained from a **genomic** clone in an Epstein-Barr virus based vector, after transfection into a human epithelial cell line, indicating the presence of effective regulatory sequences in this clone.

14/7/24 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06605822 BIOSIS NO.: 000087047984

A MAPPED SET OF GENETIC MARKERS FOR HUMAN CHROMOSOME 9

AUTHOR: LATHROP M; NAKAMURA Y; O'CONNELL P; LEPPERT M; WOODWARD S; LALOUEL J-M; WHITE R

AUTHOR ADDRESS: HOWARD HUGHES MED. INST., SALT LAKE CITY, UTAH 84132.

JOURNAL: GENOMICS 3 (4). 1988. 361-366.

FULL JOURNAL NAME: Genomics

CODEN: GNMCE

RECORD TYPE: Abstract LANGUAGE: ENGLISH

ABSTRACT: A gentic map of markers for human chromosome spanning a genetic distance of cM in males and 231 cM in fewers, has been constructed from linkage studies with 19 loci in a large panel of reference families. The markers included four classical systems previously assigned to chromosome 9, and restriction fragment length polymorphisms of two cloned genes, ABL oncogene and argininosuccinase synthetase pseudogene 3 (ASSP3). The remaining 13 marker loci, with an average herterozygosity of 42%, were defined by arbitrary DNA probes newly ascertained from genomic libraries; seven of them were variable number of tandem repeat (VNTR) loci. A subset of 7 of the 19 linked markers is proposed for a primary map that could detect linkage with a genetic defect within the covered region of chromosome 9, provided that at least 45 phase-known meioses were available for study in an affected family.

14/7/25 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
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0201896 DBA Accession No.: 96-12667

Genetic typing by capillary electrophoresis with the allelic ladder as an absolute standard - variable number tandem

repeat polymorphism detection

AUTHOR: Zhang N; Yeung E S

CORPORATE AFFILIATE: U.S.Dep.Environ. Univ.Iowa-State

CORPORATE SOURCE: Ames Laboratory, U.S. Department of the Environment,

Ames, Iowa 50011, USA.

JOURNAL: Anal.Chem. (68, 17, 2927-31) 1996

ISSN: 0003-2700 CODEN: ANCHAM

LANGUAGE: English

ABSTRACT: A genetic typing method based on capillary electrophoresis/laser-induced fluorescence (CE-LIF) was demonstrated.

Variable number tandem repeat polymorphisms in

the human D1S80 locus were studied. A pooled allelic ladder containing the 27 most common human alleles was used as the absolute standard. Extracted genomic DNA from an individual was amplified by the polymerase chain reaction (PCR). Typing could be accomplished by co-injection of the PCR product and the D1S80 ladder and then running CE. Separation by a polymer solution of polyethylene oxide in uncoated fused silica capillaries allowed high-resolution, repeated runs in the same capillary. Sensitive detection with minimal sample preparation was possible by using ethicium bromide as the intercalating dye. Statistical analysis of the data showed a high level of confidence in matching the bands, despite variations in the injection process or CE system. Further adaptation to a multiple capillary array system should allow faster throughput. (20 ref)

14/7/26 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
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0148651 DBA Accession No.: 93-06703

A low profile - examination of the use of molecular biology in DNA fingerprinting forensics

AUTHOR: Salter M; Wiggins K; Keeley R H; +Jones S T; Wilson B CORPORATE SOURCE: Metropolitan Police Forensic Science Laboratory, 109 Lambeth Road, London SE1 7LP, UK.

JOURNAL: Chem.Br. (29, 5, 419-21) 1993

CODEN: CHMBAY
LANGUAGE: English

ABSTRACT: The application of molecular biology to forensics is described. The general procedure used to produce a DNA profile is described, including (a) extraction of DNA from the sample, (b) digestion with

HinfI, (c) separation of the DNA fragments into bands by electrophoresis, transfer of the DNA band battern to a nylon membrane, (e) use of a 32P-labeled DNA probe to hybridize with the DNA, and (f) use of an X-ray film to reveal the positions of the bands that have hybridized with the probe. The DNA probes used have a base sequence complementary to a variable number tandem

repeat sequence, and can be used to identify the fragments of interest from the thousands of others on the membrane. Instead of using 32P as the label, more modern techniques use alkaline phosphatase (EC-3.1.3.1) and a chemiluminescence method of detection. Further improvements can be obtained by amplification of the DNA being analyzed using the polymerase chain reaction, and adaptation of the techniques to the profiling of mitochondrial rather than genomic DNA. (1 ref)

14/7/27 (Item 3 from file: 357) DIALOG(R) File 357: Derwent Biotechnology Abs (c) 2000 Derwent Publ Ltd. All rts. reserv.

0102806 DBA Accession No.: 90-05497

Alkaline transfer of small restriction fragments from polyacrylamide gels - Southern blot hybridization of DNA after polyacrylamide gel

electrophoresis; application in variable number

tandem repeat detection

AUTHOR: Martinson J J; Clegg J B

CORPORATE SOURCE: MRC Molecular Haematology Unit, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK.

JOURNAL: Nucleic Acids Res. (18, 5, 1307) 1990

CODEN: NARHAD LANGUAGE: English

ABSTRACT: A simple process was developed for blotting of small DNA fragments resolved by PAGE onto a cationic nylon membrane, using modified alkaline transfer. Filters could then be hybridized under standard conditions to a variety of variable number

tandem repeat (VNTR) probes. 2.5-5.0 g Genomic DNA was restricted, and PAGE loading dye was added. The PAGE gel was run, and was depurinated for 20 min, while attached to a Bind-Silane-treated plate, using 0.25 M HCl. DNA was then denatured in 0.5 M NaOH for 20 min. A blotting stack was prepared, in which the alkaline solution within the gel was used as sole transfer medium, and transfer proceeded for 4 hr. The membrane was removed by soaking the glass plate, gel and membrane in water for 10 min. Gel fragments on the membrane could be rubbed off without dislodging the DNA. Pre-hybridization and hybridization to a labeled probe were then performed. Binding of the gel to 1 plate with Bind-Silane eliminated gel distortion during blot preparation. The band sharpness and resolution enabled single repeat variation to be detected with VNTR DNA probes. Resolution was achieved

? t s14/3, ab/28-35

14/3,AB/28 (Item 1 from file: 654) DIALOG(R) File 654:US Pat. Full.

for 0.2-2.0 kb fragments. (8 ref)

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02987652

Utility

METHOD FOR CAPTURING A NUCLEIC ACID

PATENT NO.: 5,939,261

August 17, 1999 (19990817) ISSUED:

INVENTOR(s): Loewy, Zvi, Fair Lawn, NJ (New Jersey), US (United States of

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[Assignee Code(s): 47766]

APPL. NO.: 8-881,282

FILED: June 24, 1997 (19970624)

This patent application is related to the following copending U.S. patent applications: Ser. No. 08-556,036, filed Nov. 9, 1995, entitled A PARTITIONED MICROELECTRONIC DEVICE ARRAY (Zanzucchi et al.); Ser. No. 08-556,423, filed Nov. 9, 1996, entitled ELECTROKINETIC PUMPING (Zanzucchi et al.); Ser. No. 08-645,966, filed May 10, 1996, entitled ELECTROKINETIC PUMPING (Zanzucchi et al.); Ser. No. 08-483,331, filed Jun. 7, 1995, entitled METHOD AND SYSTEM FOR INHIBITING CROSS-CONTAMINATION IN FLUIDS OF COMBINATORIAL CHEMISTRY DEVICE (Demers); Ser. No. 60-009,517, filed Nov. 3, 1995, which is the priority document for a regular application filed Nov. 1, 1996, and both of which are entitled ASSAY SYSTEM (Roach et al.); Ser. No. 08-745,766, filed Nov. 8, 1996, entitled FIELD-ASSISTED SEALING (Fan et al.); Ser. No. 08-786,956, filed Jan. 22, 1997, entitled PARALLEL REACTION CASSETTE AND ASSOCIATED DEVICES (Southgate et al.); Ser. No. 08-742,971, filed Nov. 1, 1996, entitled MAGNET (McBride); Ser. No. 08-554,887, filed Nov. 9, 1995, entitled METHOD OF PRODUCING MICRO-ELECTRONIC CONDUITS (Thaler et al.); Ser. No. 08-664,780, filed Jun. 14, 1996, entitled AUTOMATED NUCLEIC ACID SOLUTION (Southgate et al.); Ser. No. 08-730,636, filed Oct. 11, 1996, entitled LIQUID DISTRIBUTION SYSTEM (Demers et al.); and Ser. No. 08-838,102, filed Apr. 15, 1997, Method For Translocating Microparticles In A Microfabricated Device (Fan et al.).

This invention was made with U.S. Government support under Contract Nos. N66001-96-C-8630 and 70NANBH1037. The U.S. Government has certain rights in this invention.

FULL TEXT:

826 lines

### ABSTRACT

The present invention relates to a method for capturing a class of nucleic acids comprising (a) providing a population of nucleic acids, wherein the population comprises the class; (b) binding a probe moiety to nucleic acids of the class, thereby forming one or more complexes, wherein the probe moiety is attached to a substrate; and (c) capturing the complex. The method can be implemented in certain embodiments in a structure comprised of one or more reservoirs, preferably wherein the reservoirs include one or more second chambers that are in communication with a first chamber. Preferably, the present invention is used to capture the class of nucleic acids that comprise regulatory elements included in a population of nucleic acids isolated from a cell, tissue, or organism. An alternative preferred embodiment of the present invention involves the capture of the class of nucleic acids that comprises certain repetitive elements included in a population of nucleic acids derived from an organism.

14/3,AB/29 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.

02788987

Utility

COMPOSITIONS FOR CHROMOSOME-SPECIFIC STAINING [Nucleic acid probes for in situ hybridization with labels]

PATENT NO.: 5,756,696

ISSUED: May 26, 1998 (19980526)

INVENTOR(s): Gray, Joe ..., Livermore, CA (California), L. (United States of

America)

Pinkel, Daniel, Walnut Creek, CA (California), US (United

States of America)

ASSIGNEE(s): Regents Of The University Of California, (A U.S. Company or

Corporation), Oakland, CA (California), US (United States of

America)

[Assignee Code(s): 13234]

APPL. NO.: 8-364,400

FILED: December 23, 1994 (19941223)

## RELATED APPLICATION

This application is a continuation of U.S. Ser. No. 08-242,075, filed May 13, 1994, now abandoned, which is a continuation of U.S. Ser. No. 08-120,190, filed Sep. 13, 1993, now abandoned, which is a continuation of U.S. Ser. No. 07-862,060, filed Apr. 2, 1992, now abandoned, which is a continuation of U.S. Ser. No. 07-444,669, filed Dec. 1, 1989, now abandoned, which is a continuation in part of U.S. Ser. No. 937,793, filed Dec. 4, 1986, now abandoned which is, in turn, a continuation in part of U.S. Ser. No. 819,314, filed Jan. 16, 1986 now abandoned by the named inventors hereof and assigned to the same assignee and claims priority in said prior filed applications.

The United States Government has rights in this invention pursuant to Contract No. W-7405-ENG-48 between the U.S. Department of Energy and the University of California, for the operation of Lawrence Livermore National Laboratory.

FULL TEXT: 3373 lines

### **ABSTRACT**

Methods and compositions for staining based upon nucleic acid sequence that employ nucleic acid probes are provided. Said methods produce staining patterns that can be tailored for specific cytogenetic analyses. Said probes are appropriate for in situ hybridization and stain both interphase and metaphase chromosomal material with reliable signals. The nucleic acid probes are typically of a complexity greater than 50 kb, the complexity depending upon the cytogenetic application. Methods are provided to disable the hybridization capacity of shared, high copy repetitive sequences and/or remove such sequences to provide for useful contrast. Still further methods are provided to produce chromosome-specific staining reagents which are made specific to the targeted chromosomal material, which can be one or more whole chromosomes, one or more regions on one or more chromosomes, subsets of chromosomes and/or the entire genome. Probes and test kits are provided for use in tumor cytogenetics, in the detection of disease related loci, in analysis of structural abnormalities, such as translocations, and for biological dosimetry. Further, methods and prenatal test kits are provided to stain targeted chromosomal material of fetal cells, including fetal cells obtained from maternal blood. Still further, the invention detect and analyse chromosomal for automated means to provides abnormalities.

14/3,AB/30 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.

02788602

Utility
SEQUENCE OF HUMAN DOPAMINE TRANSPORTER CDNA

PATENT NO.: 5,756,307

ISSUED: May 26, 1 (19980526)

INVENTOR(s): Uhl, George R., Towson, MD (Maryland), US (United States of

America)

Vandenbergh, David, Baltimore, MD (Maryland), US (United

States of America)

ASSIGNEE(s): The United States of America as represented by the Department

of Health and Human Services, (A U.S. Government Agency), Washington, DC (District of Columbia, US (United States of

America)

[Assignee Code(s): 6814]

APPL. NO.: 8-301,722

FILED: September 07, 1994 (19940907)

## RELATED APPLICATIONS

This application is a continuation of application Ser. No. 07-889,723 filed on Jun. 1, 1992, now abandoned, which is a continuation-in-part of application Ser. No. 07-762,132 filed on Sep. 20, 1991, U.S. Pat. No. 5,312,734.

FULL TEXT:

1776 lines

### ABSTRACT

The cloning and characterization of a human dopamine transporter (HUDAT) cDNA is described. RFLP analysis is used to determine the distribution of HUDAT alleles in two ethic backgrounds. The means by which the association between HUDAT alleles and behavioral disorders which have altered HUDAT expression as a basis for their etiology is discussed. Methods for evaluating the expression of HUDAT are described.

14/3, AB/31 (Item 4 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02745507

Utility

VNTR PROBES AND METHODS OF USING THEREOF [Genetic identification]

PATENT NO.: 5,716,786

ISSUED: February 10, 1998 (19980210)
INVENTOR(s): Buard, Jerome, Paris, FR (France)

Gauquier, Dominique, St Mande, FR (France)

Vergnaud, Gilles, Paris, FR (France)

ASSIGNEE(s): L'Etat Français, represente par le Delegue Ministeriel pour

l'Armement, (A Non-U.S. Government Entity), Armees, FR (France)

[Assignee Code(s): 7029]

APPL. NO.: 8-690,129

FILED: July 31, 1996 (19960731)

PRIORITY: 93-12923, FR (France), October 29, 1993 (19931029)

This application is a division of application Ser. No. 08-331,910, filed Oct. 31, 1994, now U.S. Pat. No. 5,573,912.

FULL TEXT: 679 lines

# ABSTRACT

According to the process of the invention, sets of restriction fragments from the DNA of an individual are prepared, these restriction fragments

being separated by siz Probes are prepared by enzymation hydrolysis of DNA from a genome bank the species to which this dividual belongs, separation of the fragments obtained as a function of their size, labeling these probes and placing them in contact, under hybridization conditions, with the aforementioned sets of restriction fragments. Finally, selection is made of the probes (capable of hybridizing with said set of restriction fragments) which do not give hybridization profiles identical to those obtained with known probes recognizing variable number tandem repeat regions. Applications for the probes thus obtained include, particularly, processes for identifying an individual, consanguinity testing, and investigating the origin of a seed.

14/3,AB/32 (Item 5 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02724581

Utility

DETECTING GENETIC PREDISPOSITION FOR OSTEOPOROSIS [Isolation genomic Dna; determination allelic pattern]

PATENT NO.: 5,698,399

ISSUED: December 16, 1997 (19971216)

INVENTOR(s): Duff, Gordon W., 18 Ashgate Road, Sheffield, S10 3BZ, S Yorks,

GB (United Kingdom). England

Russell, Graham, Ronksley Farm Hollow Meadows, Sheffield,

South Yorks S6 6GH, GB (United Kingdom). England

Eastell, Richard, 289 Ringinglow Road, Sheffield, S11 7PZ, GB

(United Kingdom).England [Assignee Code(s): 68000]

EXTRA INFO: Assignment transaction [Reassigned], recorded December 8,

1997 (19971208)

Assignment transaction [Reassigned], recorded July 28,

1998 (19980728)

APPL. NO.: 8-628,282

FILED: April 05, 1996 (19960405)

FULL TEXT: 632 lines

## ABSTRACT

The present invention relates to methods of predicting the risk of osteoporosis. Specifically, the methods comprise isolating **genomic** DNA from an individual and determining an allelic pattern for IL-1 receptor antagonist (IL-1ra) in the **genomic** DNA. The identification of at least one copy of allele 2 indicates increased susceptibility to osteoporosis.

14/3,AB/33 (Item 6 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02588755

Utility

PROCESS OF SELECTING AND/OR OBTAINING PROBES CAPABLE OF DETECTING NEW VARIABLE NUMBER TANDEM REPEAT REGIONS

PATENT NO.: 5,573,912

ISSUED: November 12, 1996 (19961112)

Vergnaud, Gilles, Paris, FR (France)

ASSIGNEE(s): Etat Francais represente par le Deleque General pour

L'Armement, (A Non-U.S. Government Entity), Armees, FR (France)

[Assignee ode(s): 7029]
[EXTRA INFO: Assignmen ransaction [Reassigned], record April 23,

1997 (19970423)

8-331,910 APPL. NO.:

October 31, 1994 (19941031) FILED:

93-12923, FR (France), October 29, 1993 (19931029) PRIORITY:

FULL TEXT:

727 lines ABSTRACT

According to the process of the invention, sets of restriction fragments from the DNA of an individual are prepared, these restriction fragments being separated by size. Probes are prepared by enzymatic hydrolysis of DNA from a genome bank of the species to which this individual belongs, separation of the fragments obtained as a function of their size, labeling these probes and placing them in contact, under hybridization conditions, with the aforementioned sets of restriction fragments. Finally, selection is made of the probes (capable of hybridizing with said set of restriction fragments) which do not give hybridization profiles identical to those obtained with known probes recognizing variable number tandem repeat regions. Applications for the probes thus obtained include, particularly, processes for identifying an individual, consanguinity testing, and investigating the origin of a seed.

-

14/3,AB/34 (Item 7 from file: 654) DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02468366

Utility

PROCESS FOR TESTING GENE-DISEASE ASSOCIATIONS

PATENT NO.: 5,464,742

November 07, 1995 (19951107) ISSUED:

INVENTOR(s): Swift, Michael R., 1004 Mt. Carmel Church Rd., Chapel Hill, NC

(North Carolina), US (United States of America)

Kupper, Lawrence L., Chapel Hill, NC (North Carolina), US

(United States of America)

Chase, Charles L., Chapel Hill, NC (North Carolina), US

(United States of America)

ASSIGNEE(s): Swift, Michael R, (A U.S. Individual), Scarsdale, NY (New

York), US (United States of America)

- [Assignee Code(s): 68000]

8-137,898 APPL. NO.:

October 19, 1993 (19931019) FILED:

This application is a continuation of application Ser. No. 07-562,007, filed Aug. 2, 1990, now abandoned.

The United States Government has rights in this invention pursuant to National Institutes of Health Grants No. CA 14235 and HD 03110, awarded by the U.S. Department of Health and Human Services.

1131 lines FULL TEXT:

# ABSTRACT

The present invention describes a process to test the association of an allele and a disease, especially a non-Mendelian disease. The process involves a comparison of the proportion of test individuals who have the disease and carry the allele from a set of families in which the allele is present and the proportion of test individuals expected to carry the allele if there is no association between the gene and the discuse.

14/3,AB/35 (Item 8 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02427349

Utility

REPEAT SEQUENCE CHROMOSOME SPECIFIC NUCLEIC ACID PROBES AND METHODS OF PREPARING AND USING

[ Primer directed DNA amplification using degenerate primers to isolate efficiently chromosome-specific repeated DNA]

PATENT NO.: 5,427,932

ISSUED: June 27, 1995 (19950627)

INVENTOR(s): Weier, Heinz-Ulrich G., Tracy, CA (California), US (United

States of America)

Gray, Joe W., San Francisco, CA (California), US (United

States of America)

ASSIGNEE(s): Reagents of the University of California, (A U.S. Company or

Corporation), Oakland, CA (California), US (United States of

America)

[Assignee Code(s): 13234]

APPL. NO.: 7-858,124

FILED: March 26, 1992 (19920326)

### RELATED APPLICATIONS

This application is a continuation-in-part application of U.S. Ser. No. 07-683,441 filed Apr. 9, 1991, now abandoned. Priority in said prior filed applications is herein claimed.

The United States Government has rights in this invention pursuant to Contract No. W-7405-ENG-48 between the United States Department of Energy and the University of California for the operation of Lawrence Livermore National Laboratory.

FULL TEXT: 2094 lines

# ABSTRACT

A primer directed DNA amplification method to isolate efficiently chromosome-specific repeated DNA wherein degenerate oligonucleotide primers are used is disclosed. The probes produced are a heterogeneous mixture that can be used with blocking DNA as a chromosome-specific staining reagent, and/or the elements of the mixture can be screened for high specificity, size and/or high degree of repetition among other parameters. The degenerate primers are sets of primers that vary in sequence but are substantially complementary to highly repeated nucleic acid sequences, preferably clustered within the template DNA, for example, pericentromeric satellite repeat sequences. The template DNA is preferably chromosome-specific. Exemplary primers and probes are disclosed. The probes of this invention can be used to determine the number of chromosomes of a specific type in metaphase spreads, in germ line and/or somatic cell interphase nuclei, micronuclei and/or in tissue sections. Also provided is a method to select arbitrarily repeat sequence probes that can be screened for chromosome-specificity. ? logoff

17apr00 20:24:12 User233835 Session D393.3 \$1.32 0.413 DialUnits File155

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Logging in to Dialog Trying 3106900061...Open DIALOG INFORMATION SERVICES PLEASE LOGON: \*\*\*\*\* ENTER PASSWORD: □t8401cpg \*\*\*\*\* Welcome to DIALOG Dialog leel 00.03.02D Lat logoff: 17apr00 20:24:12 Logon file001 18apr00 12:50:01 \*\*\* ANNOUNCEMENT \*\*\* NEW FILE RELEASED \*\*\*New Scientit (File 369) \*\*\*Newweek Flltext (File 482) \*\*\*WIPO/PCT Patent Flltext (File 349) UPDATING RESUMED \*\*\*Bridge World Market New (File 609,809) \*\*\*Fort Worth Star-Telegram (File 427) \*\*\*Federal New Serice (File 660) \*\*\*Kana Cit Star (File 147) RELOADED \*\*\*AIDSLINE (File 157) \*\*\*Book in Print (File 470) \*\*\*Kompa Latin America (File 586) >>>Get immediate new with Dialog' Firt Releae new erice. Firt Releae pdate major newwire □dialog databases within 15 minutes of transmission over the wire. First Release provides full Dialog searchability and full-text features. To search First Release files in OneSearch simply BEGIN FIRST for coverage from Dialog's broad spectrum of news wires. >>> Enter BEGIN HOMEBASE for Dialog Announcements <<< >>> of new databases, price changes, etc. \*\*\*\* 1:ERIC 1966-2000/Feb File (c) format only 2000 The Dialog Corporation 1: File has been reloaded. See HELP NEWS 1. Set Items Description ? b 410 >>>'IALOG' not recognized as set or accession number

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 File 5:Biosis Previews(R) 1969-2000/Apr W3
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 File 399:CA SEARCH(R) 1967-2000/UD=13216
         (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
 File 357: Derwent Biotechnology Abs 1982-2000/Apr B2
         (c) 2000 Derwent Publ Ltd
 File 654:US Pat.Full. 1990-2000/Apr 11 (c) format only 2000 The Dialog Corp.
*File 654: Reassignment data current through 12/06/1999 recordings.
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         29747 TAG
256010 FRAGMENT
82918 OLIGONUCLEOTIDE
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          160329 POLYMORPHISM
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          54940 TANDEM
         135318 REPEAT
            461 VARIABLE (W) NUMBER (W) TANDEM (W) REPEAT
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         (Item 1 from file: 654)
4/6/1
03084775
METHODS OF DETECTING ALZHEIMER'S DISEASE
                1496 lines
FULL TEXT:
         (Item 2 from file: 654)
4/6/2
03084769
METHODS AND COMPOSITIONS FOR ENHANCING SENSITIVITY IN THE ANALYSIS OF
BIOLOGICAL-BASED ASSAYS
FULL TEXT:
                 5884 lines
          (Item 3 from file: 654)
4/6/3
03067992
DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR ELECTROPHORESIS
                 1867 lines
FULL TEXT:
          (Item 4 from file: 654)
4/6/4
02983945
DETECTION OF HYPERMUTABLE NUCLEIC ACID SEQUENCE IN TISSUE
                 1815 lines
FULL TEXT:
         (Item 5 from file: 654)
4/6/5
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
                 4623 lines
FULL TEXT:
          (Item 6 from file: 654)
4/6/6
02893130
DIAGNOSIS OF RETINOBLASTOMA
FULL TEXT:
                1223 lines
4/6/7
          (Item 7 from file: 654)
02881547
MULTIPLEX AMPLIFICATION OF SHORT TANDEM REPEAT LOCI
                 3051 lines
FULL TEXT:
          (Item 8 from file: 654)
4/6/8
02871149
GENE SEQUENCE FOR SPINOCEREBELLAR ATAXIA TYPE 1 AND METHOD FOR DIAGNOSIS
[For diagnosis of autosomal dominant spinocerebellar ataxia type 1 gene]
FULL TEXT:
                 4786 lines
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4/6/9 (Item 9 from file: 654)

02846423

METHOD OF CHARACTERISATION

[Amplification of tandemly repeated region of genomic DNA, separation

of set of amplification products to provide sample code]

FULL TEXT: 3543 lines

4/6/10 (Item 10 from file: 654)

02846421

COMPOSITIONS AND USES THEREOF IN THE DIAGNOSIS OF PSORIASIS

[Screening for psoriasis susceptibility by determining in a nucleic acid sample the presence of a polymorphic marker linked with a gene for interleukin enhancer binding factor]

FULL TEXT: 2235 lines

4/6/11 (Item 11 from file: 654)

02816905

APC (ADENOMATOUS POLYOSIS COLI) PROTEIN

[Hybrid]

FULL TEXT: 3924 lines

4/6/12 (Item 12 from file: 654)

02816663

ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI

[Detecting Dna sequernces]
FULL TEXT: 1268 lines

4/6/13 (Item 13 from file: 654)

02716697

APC ANTIBODIES

FULL TEXT: 4328 lines

4/6/14 (Item 14 from file: 654)

02698037

ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI

[ Detection of alleles by comparing three polymerase chain reaction co-amplified short tandem DNA repeat sequences with allelic ladder]

FULL TEXT: 1262 lines

4/6/15 (Item 15 from file: 654)

02668237

DETECTION OF INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL

CANCER OF HUMANS

FULL TEXT: 4452 lines

4/6/16 (Item 16 from file: 654)

02616589

ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI

[Markers for detection of specific DNA sequences, also kits]

FULL TEXT: 1261 lines

4/6/17 (Item 17 from file: 654)

02451514

CHROMOSOME 14 AND FAMILIAL ALZHEIMERS DISEASE GENETIC MARKERS AND ASSAYS

FULL TEXT: 3467 lines

(Item 18 from file: 654) 4/6/18 02409494 GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER TANDEM REPEAT LOCI 2125 lines FULL TEXT: 4/6/19 (Item 19 from file: 654) 02357021 DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS FULL TEXT: 1738 lines (Item 20 from file: 654) 4/6/20 01913496 GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER TANDEM REPEAT LOCI [IDENTIFICATION OF CLONED DNA SEQUENCES] FULL TEXT: 2145 lines ? ds Items Description Set S1 2820 GENOMIC AND TAG AND FRAGMENT AND OLIGONUCLEOTIDE S2 464 S1 AND POLYMORPHISM 20 S3 20 RD (unique items) S4

S2 AND (VNTR OR (VARIABLE(W) NUMBER(W) TANDEM(W) REPEAT)) ? t s4/3, ab/5, 7, 9, 14-20

4/3, AB/5(Item 5 from file: 654) DIALOG(R) File 654:US Pat. Full. (c) format only 2000 The Dialog Corp. All rts. reserv.

02893131

Utility

METHOD OF CHARACTERISATION OF GENOMIC DNA

PATENT NO.: 5,853,989

December 29, 1998 (19981229) ISSUED:

INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom). Great

Britian

Little, Stephen, Chester, GB (United Kingdom). Great Britian Ferrie, Richard Mark, Cheshire, GB (United Kingdom). Great

Brownie, Jannine, Cheshire, GB (United Kingdom). Great Britian

ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London,

GB (United Kingdom)

[Assignee Code(s): 32757]

APPL. NO.: 8-643,181

May 06, 1996 (19960506) FILED:

9118371, GB (United Kingdom), August 27, 1991 (19910827) PRIORITY:

9119089, GB (United Kingdom), September 6, 1991 (19910906) 9124636, GB (United Kingdom), November 20, 1991 (19911120) 9207379, GB (United Kingdom), April 3, 1992 (19920403) 9212627, GB (United Kingdom), June 15, 1992 (19920615) 9212881, GB (United Kingdom), June 17, 1992 (19920617)

This application is a continuation-in-part of application of Ser. No. 08-418,859 filed Apr. 5, 1995 which is a continuation of 07-935,107, filed Aug. 26, 1992 now abandoned.

4623 nes

#### ABSTRACT

The present invention relates generally to a method of characterizing a sample of **genomic** DNA and to nucleotide sequences employed in the method as well as kits comprising these. In particular the invention involves the use of primers which selectively prime specific type(s) of internal repeat unit in a tandemly repeated region. The method of the invention is particularly useful in forensic or paternity studies and provides individual sample codes suitable for computerized storage on, and retrieval from, a database.

4/3, AB/7 (Item 7 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02881547

Utility

MULTIPLEX AMPLIFICATION OF SHORT TANDEM REPEAT LOCI

PATENT NO.: 5,843,660

ISSUED: December 01, 1998 (19981201)

INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States

of America)

Micka, Katherine A., Oregon, WI (Wisconsin), US (United States

of America)

Rabbach, Dawn R., DeForest, WI (Wisconsin), US (United States

of America)

ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison,

WI (Wisconsin), US (United States of America)

[Assignee Code(s): 18871]

APPL. NO.: 8-632,575

FILED: April 15, 1996 (19960415)

This application is a continuation-in-part of U.S. patent application Ser. No. 08-316,544, filed Sep. 30, 1994. The entire disclosure of that parent application is incorporated by reference herein.

FULL TEXT: 3051 lines

# ABSTRACT

The present invention is directed to the simultaneous amplification of multiple distinct genetic loci using PCR or other amplification systems to determine in one reaction the alleles of each of the loci contained within the multiplex.

4/3,AB/9 (Item 9 from file: 654)

DIALOG(R) File 654:US Pat. Full.

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02846423

Utility

METHOD OF CHARACTERISATION

[Amplification of tandemly repeated region of **genomic** DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235

ISSUED: September 22, 1998 (19980922)

INVENTOR(s): Jeffreys ec John, Leicester, GB (United ingdom). England ASSIGNEE(s): Zeneca Lieck, (A Non-U.S. Company or Coloration), London, GB (United Kingdom) England ration), London,

[Assignee Code(s): 32757]

8-418,859 APPL. NO.:

April 05, 1995 (19950405) FILED:

9118371, GB (United Kingdom), August 27, 1991 (19910827) PRIORITY:

9119089, GB (United Kingdom), September 6, 1991 (19910906) 9124636, GB (United Kingdom), November 20, 1991 (19911120) 9207379, GB (United Kingdom), April 3, 1992 (19920403) 9212627, GB (United Kingdom), June 15, 1992 (19920615) 9212881, GB (United Kingdom), June 17, 1992 (19920617)

This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT: 3543 lines

### ABSTRACT

A method of characterizing a test sample of genomic DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.

(Item 14 from file: 654) 4/3, AB/14DIALOG(R) File 654:US Pat. Full.

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02698037

Utility

ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI

[ Detection of alleles by comparing three polymerase chain reaction co-amplified short tandem DNA repeat sequences with allelic ladder]

PATENT NO.: 5,674,686

October 07, 1997 (19971007) ISSUED:

INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States

of America)

Puers, Christoph, Madison, WI (Wisconsin), US (United States

of America)

ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison,

WI (Wisconsin), US (United States of America)

[Assignee Code(s): 18871]

EXTRA INFO: Assignment transaction [Reassigned], recorded October 13,

1998 (19981013)

APPL. NO.: 8-515,236

August 15, 1995 (19950815) FILED:

This is a divisional of application Ser. No. 08-219,633, filed Mar. 28, 1994.

FULL TEXT: 1262 lines

ABSTRACT

The present invention is directed to an assay system kit and a process for detecting at let one short tandem repeat strence from DNA at a specific locus utilizing an allelic ladder containing at least two short tandem repeat sequences of the same lengths as two or more known alleles for the locus.

(Item 15 from file: 654) 4/3,AB/15 DIALOG(R) File 654:US Pat. Full. (c) format only 2000 The Dialog Corp. All rts. reserv.

02668237

Utility

DETECTION OF INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL CANCER OF HUMANS

PATENT NO.: 5,648,212

July 15, 1997 (19970715) ISSUED:

INVENTOR(s): Albertsen, Hans, Salt Lake City, UT (Utah), US (United States

of America)

Anand, Rakesh, Cheshire, GB (United Kingdom). England

Carlson, Mary, Salt Lake City, UT (Utah), US (United States of

America)

Groden, Joanna, Salt Lake City, UT (Utah), US (United States

of America)

Hedge, Philip John, Cheshire, GB (United Kingdom). England Joslyn, Geoff, Salt Lake City, UT (Utah), US (United States of

America)

Kinzler, Kenneth, Baltimore, MD (Maryland), US (United States

of America)

Markham, Alexander, Cheshire, GB (United Kingdom). England

Nakamura, Yusuke, Tokyo, JP (Japan)

Thliveris, Andrew, Salt Lake City, UT (Utah), US (United

States of America)

Vogelstein, Bert, Baltimore, MD (Maryland), US (United States

of America)

White, Raymond L., Salt Lake City, UT (Utah), US (United

States of America)

ASSIGNEE(s): Japanese Foundation for Cancer Research Cancer Institute, (A Non-U.S. Company or Corporation), Tokyo, JP (Japan)

The John Hopkins University, (A U.S. Company or Corporation),

Baltimore, MD (Maryland), US (United States of America)

University of Utah, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)

Zeneca Limited, (A Non-U.S. Company or Corporation), Cheshire,

GB (United Kingdom) England

[Assignee Code(s): 12629; 32757; 39884; 88042]

APPL. NO.: 8-289,548

August 12, 1994 (19940812) FILED:

9100962, GB (United Kingdom), January 16, 1991 (19910116) PRIORITY:

9100963, GB (United Kingdom), January 16, 1991 (19910116)

9100974, GB (United Kingdom), January 16, 1991 (19910116)

9100975, GB (United Kingdom), January 16, 1991 (19910116)

This application is a division of application Ser. No. 07-741,940, filed Aug. 8, 1991, which issued as U.S. Pat. No. 5,352,775.

The U.S. Government has a paid-up license in this invention and the right in limited circumstances to require the patent owner to license others on reasonable terms as provided for by the terms of grants awarded by the National Institutes of Health.

FULL TEXT: 4452 lines Methods are provided for assessing mutations of the APC gene in human tissues and body samples. APC mutations are found in familial adenomatous polyposis patients as well as in sporadic colorectal cancer patients. APC is expressed in most normal tissues. APC is a tumor suppressor.

4/3, AB/16 (Item 16 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02616589

Utility

ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI

[Markers for detection of specific DNA sequences, also kits]

PATENT NO.: 5,599,666

ISSUED: February 04, 1997 (19970204)

INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States

of America)

Puers, Christoph, Madison, WI (Wisconsin), US (United States

of America)

ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison,

WI (Wisconsin), US (United States of America)

[Assignee Code(s): 18871]

APPL. NO.: 8-219,633

FILED: March 28, 1994 (19940328)

FULL TEXT: 1261 lines

### ABSTRACT

The present invention is directed to an assay system, a kit and a process for detecting at least one short tandem repeat sequence from DNA at a specific locus utilizing an allelic ladder containing at least two short tandem repeat sequences of the same lengths as two or more known alleles for the locus.

4/3, AB/17 (Item 17 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02451514

Utility

CHROMOSOME 14 AND FAMILIAL ALZHEIMERS DISEASE GENETIC MARKERS AND ASSAYS

PATENT NO.: 5,449,604

ISSUED: September 12, 1995 (19950912)

INVENTOR(s): Schellenberg, Gerard D., Seattle, WA (Washington), US (United

States of America)

Bird, Thomas D., Seattle, WA (Washington), US (United States

of America)

Wijsman, Ellen M., Seattle, WA (Washington), US (United States

of America)

ASSIGNEE(s): University of Washington, (A U.S. Company or Corporation),

Seattle, WA (Washington), US (United States of America)

[Assignee Code(s): 2937]

APPL. NO.: 7-964,151

FILED: October 21, 1992 (19921021)

This invention was made with government support under grant AG08017 awarded by the National Institute on Aging and grant R01MH43240 awarded by

FULL TEXT:

3467 lines

## ABSTRACT

Method for isolating a DNA segment indicative of an Alzheimer's disease trait in a family population, wherein said family population consists essentially of a plurality of blood relatives of an individual having a chromosome 14 Alzheimer's disease trait, by: preparing a test sample of immobilized separated genomic DNA fragments from a plurality of the blood relatives, contacting each of the test samples with a test oligonucleotide under conditions permitting hybridization of complementary single stranded DNA molecules, wherein the oligonucleotide is complementary with at least a portion of a genetic marker located between band q11.2 and band q32.1 in chromosome 14, identifying a plurality of hybridized molecules so formed as alleles of the genetic marker in the family population, identifying one of the genetic marker alleles as indicative of the Alzheimer's disease trait in the family population by either determining by pedigree analysis a segregation value for each of the genetic markers alleles and the Alzheimer's disease trait, and selecting an indicative genetic marker allele that co-segregates with the Alzheimer's disease trait in the family population, or measuring genetic linkage between each of the genetic marker alleles and the Alzheimer's disease trait, and selecting a genetic marker allele as indicative of the Alzheimer's disease trait in the family population if the selected genetic marker allele has a maximal LOD score of at least 3 at a recombination fraction of about 0.0 to about 0.1 for genetic linkage with the Alzheimer's disease trait in the family population, and isolating a chromosome 14 DNA segment containing the indicative genetic marker allele.

4/3,AB/18 (Item 18 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) format only 2000 The Dialog Corp. All rts. reserv.

02409494

Utility

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER TANDEM REPEAT LOCI

PATENT NO.: 5,411,859

ISSUED: May 02, 1995 (19950502)

INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United

States of America)

Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States

of America)

O'Connell, Peter, Salt Lake City, UT (Utah), US (United States

of America)

Midvale, Salt Lake City, UT (Utah), US (United States of

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Leppert, Mark F., Salt Lake City, UT (Utah), US (United States

of America)

ASSIGNEE(s): University of Utah Research Foundation, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of

America)

[Assignee Code(s): 88042]

EXTRA INFO: Assignment transaction [Reassigned], recorded April 29,

1998 (19980429)

Assignment transaction [Reassigned], recorded February 26,

1999 (19990226)

APPL. NO.: 7-728,751

FILED: June 10, 1991 (19910610)

This application is a continuation of application Ser. No. 07-597,039, filed Oct. 15, 1990, now abandoned, which is divisional of application Ser. No. 07-307,820, filed Feb. 8, 1989, now U.S. Pat. No. 4,963,663, which is a continuation-in-part of application Ser. No. 07-288,835, filed Dec. 23, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-282,141, filed Dec. 9, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-157,962, filed Feb. 18, 1988, now abandoned.

FULL TEXT:

2125 lines

### ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize **VNTR** loci have been isolated from a cosmid library and characterized.

4/3, AB/19 (Item 19 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

02357021

Utility

DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS

PATENT NO.: 5,364,759

ISSUED: November 15, 1994 (19941115)

INVENTOR(s): Caskey, Charles T., Houston, TX (Texas), US (United States of

America)

Edwards, Albert O., Houston, TX (Texas), US (United States of

America)

ASSIGNEE(s): Baylor College of Medicine, (A U.S. Company or Corporation),

Houston, TX (Texas), US (United States of America)

[Assignee Code(s): 6345]

EXTRA INFO: Reexamined, certified November 18, 1997 (19971118)

Reexamined, certified July 20, 1999 (19990720)

APPL. NO.: 7-647,655

FILED: January 31, 1991 (19910131)

FULL TEXT: 1738 lines

ABSTRACT

The present invention relates to a DNA profiling assay for detecting polymorphisms in a short tandem repeat. The method includes the steps of extracting DNA from a sample to be tested, amplifying the extracted DNA and identifying the amplified extension products for each different sequence. Each different sequence is differentially labeled. In the method, internal and external standards can also be used. The method is applicable to a wide variety of forensic and medical samples, including blood, semen, vaginal swaps, tissue, hair, saliva, urine and mixtures of body fluids. A short tandem repeat sequence which can be characterized by the formula (A sub w G sub x T sub y C sub z) sub n, wherein A, G, T and C represent the nucleotides, w, x, y and z represent the number of nucleotide and range from 0 to 7 and the sum of w+x+y+z ranges from 3 to 7 and n represents the repeat number and ranges from 5 to 50. The labels can be from a variety of groups, including fluorescers, radioisotopes, chemiluminescers, stains, enzymes and antibodies. Also described is a kit. Further, a method of

detecting the polymorphic short tandem repeats complising the steps of weither searching the repeats in a data hase or comparing oligonucleotides and searching for the repeats in a genetic library.

4/3,AB/20 (Item 20 from file: 654)

DIALOG(R) File 654:US Pat. Full.

(c) format only 2000 The Dialog Corp. All rts. reserv.

01913496

Utility

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF VARIABLE NUMBER

TANDEM REPEAT LOCI

[IDENTIFICATION OF CLONED DNA SEQUENCES]

PATENT NO.: 4,963,663

ISSUED: October 16, 1990 (19901016)

INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United

States of America)

Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States

of America)

O'Connell, Peter, Midvale, UT (Utah), US (United States of

America)

Leppert, Mark F., Salt Lake City, UT (Utah), US (United States

of America)

ASSIGNEE(s): University of Utah, (A U.S. Company or Corporation ), Salt

Lake City, UT (Utah), US (United States of America)

[Assignee Code(s): 88042]

EXTRA INFO: Assignment transaction [Reassigned], recorded March 3,

1992 (19920303)

Assignment transaction [Reassigned], recorded April 29,

1998 (19980429)

Assignment transaction [Reassigned], recorded February 26,

1999 (19990226)

APPL. NO.: 7-307,820

FILED: February 08, 1989 (19890208)

# CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation-in-part of application Ser. No. 288,835, filed Dec. 23, 1988 which is a continuation-in-part of application Ser. No. 282,141, filed Dec. 9, 1988 which is a continuation-in-part of application Ser. No. 157,962 filed Feb. 18, 1988.

FULL TEXT:

2145 lines

### ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize **VNTR** loci have been isolated from a cosmid library and characterized. ? ds

Set	Items	Description
S1	2820	GENOMIC AND TAG AND FRAGMENT AND OLIGONUCLEOTIDE
S2	464	S1 AND POLYMORPHISM
s3	20	S2 AND (VNTR OR (VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT))
S4	20	RD (unique items)
? rd s2		

>>>Duplicate detection is not supported for File 654.

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>>>Records from unsuppled ed files will be retained in
...examined 50 records
                        (50)
...examined 50 records
                       (100)
...examined 50 records
                       (150)
...examined 50 records
                       (200)
...examined 50 records
                       (250)
...examined 50 records
...examined 50 records
                        (350)
...examined 50 records
                       (400)
...examined 50 records
                       (450)
...completed examining records
Processing
            464 RD S2 (unique items)
   S5
? t s5/6/1-20
 5/6/1
          (Item 1 from file: 654)
03107586
HUMAN T CELL REACTIVE FELINE PROTEIN (TRFP) ISOLATED FROM HOUSE DUST AND
USES THEREFOR
FULL TEXT:
                 5293 lines
          (Item 2 from file: 654)
 5/6/2
03107462
OB POLYPEPTIDES AS MODULATORS OF BODY WEIGHT
FULL TEXT:
                 7560 lines
          (Item 3 from file: 654)
 5/6/3
03107334
COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
DISEASE
FULL TEXT:
                 5804 lines
 5/6/4
          (Item 4 from file: 654)
03107314
METHOD FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCES
              4156 lines
FULL TEXT:
 5/6/5
          (Item 5 from file: 654)
03104538
ISOLATED TRBP POLYPEPTIDES AND USES THEREFOR
FULL TEXT: 4296 lines
           (Item 6 from file: 654)
 5/6/6
03104388
UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE LECTINS, DECTIN-1 AND DECTIN-2;
COMPOSITIONS AND USES THEREOF
                  6726 lines
FULL TEXT:
          (Item 7 from file: 654)
 5/6/7
03104262
ARF-P19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
FULL TEXT:
                  4924 lines
          (Item 8 from file: 654)
 5/6/8
 03104258
 POLYNUCLEOTIDES ENCODING INSULIN HOMOLOG ZINS3
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FULL TEXT: 2195 nes

5/6/9 (Item 9 from file: 654)

03104239

DIAGNOSIS AND TREATMENT OF GLAUCOMA

FULL TEXT: 1271 lines

5/6/10 (Item 10 from file: 654)

03104227

MATERIALS AND METHODS RELATING TO THE IDENTIFICATION AND SEQUENCING OF THE

BRCA2 CANCER SUSCEPTIBILITY GENE AND USES THEREOF

FULL TEXT: 9257 lines

5/6/11 (Item 11 from file: 654)

03104034

METHOD FOR DETECTING B. BURGDORFERI INFECTION

FULL TEXT: 951 lines

5/6/12 (Item 12 from file: 654)

03104024

PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE

FULL TEXT: 4757 lines

5/6/13 (Item 13 from file: 654)

03101292

EPSTEIN BARR VIRUS INDUCED GENES

FULL TEXT: 2093 lines

5/6/14 (Item 14 from file: 654)

03101287

COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS,

INCLUDING OBESITY

FULL TEXT: 4382 lines

5/6/15 (Item 15 from file: 654)

03101030

PROSTATE/COLON TUMOR SUPPRESSOR GENE LOCATED ON HUMAN CHROMOSOME 8

FULL TEXT: 3676 lines

5/6/16 (Item 16 from file: 654)

03100997

MAMMALIAN PRO-APOPTOTIC BOK GENES AND THEIR USES

FULL TEXT: 1936 lines

5/6/17 (Item 17 from file: 654)

03100982

CSAK-3 NUCLEIC ACID MOLECULES AND USES THEREFOR

FULL TEXT: 5198 lines

5/6/18 (Item 18 from file: 654)

03097788

VASCULAR ENDOTHELIAL GROWTH FACTOR 2

FULL TEXT: 5072 lines

(Item 19 f file: 654) 5/6/19 • • • **.** • 03094632

ISOLATED NUCLEIC ACID ENCODING TRBP

FULL TEXT: 4285 lines

(Item 20 from file: 654) 5/6/20

03094618

POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-O-SULFOTRANSFERASE AND DNA ENCODING

THE SAME

FULL TEXT:

1985 lines

? logoff

18apr00 12:58:00 User233835 Session D394.3

\$0.57 0.179 DialUnits File155

\$0.57 Estimated cost File155

\$1.11 0.198 DialUnits File5

\$1.11 Estimated cost File5

\$2.25 0.179 DialUnits File399

\$2.25 Estimated cost File399

\$1.02 0.087 DialUnits File357

\$1.02 Estimated cost File357

\$7.72 1.309 DialUnits File654

\$0.00 40 Type(s) in Format 6 \$9.50 10 Type(s) in Format 4 (UDF)

\$9.50 50 Types

\$17.22 Estimated cost File654

OneSearch, 5 files, 1.952 DialUnits FileOS

\$0.30 TYMNET

\$22.47 Estimated cost this search

\$23.03 Estimated total session cost 2.156 DialUnits

Logoff: level 00.03.02 D 12:58:00